

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 47/1833

TO: Ginny Portner Location: 3b02/3c18

Tuesday, November 29, 2005

Art Unit: 1645

Phone: 571-272-0862

Serial Number: 09 / 904994

From: Jan Delaval

**Location: Biotech-Chem Library** 

Remsen 1a51

Phone: 571-272-2504

jan.delaval@uspto.gov

Search Notes		
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#### STIC-Biotech/ChemLib

From:

Portner, Ginny

Sent:

Wednesday, November 16, 2005 6:32 PM

To:

STIC-Biotech/ChemLib

Subject: 09/904,994

please search SEQ ID NO 1, 2 and 3. thanks

Ginny Portner Remsen Building Art Unit 1645 Room E03, B02 (571) 272-0862

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Jan (DY



## STIC SEARCH RESULTS FEEDBACK FORM

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Voluntary Results Feedback Form

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 22507, Remsen 1d86

### 

Results verified the lack of relevant prior art (helped determine patentability).

Results were not useful in determining patentability or understanding the invention.

Comments:

Dies off or send completed forms to STICE to the Chem Library CM1 – Cite. Desk



#### November 2005

Published\_Applications Nucleic Acid and Published\_Applications Amino Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic Acid Published\_Applications produce two sets of results, with the extensions srnpbm (Published\_Applications\_NA\_Main) and .rnpbn (Published\_Applications\_NA\_New).

Searches run against Amino Acid Published\_Applications produce two sets of results, with the extensions .rapbm (Published\_Applications\_AA\_New).

ARO61045 Sequence AR164678 Sequence AR349306 Sequence AR349306 Sequence X69080 H. Felis ure X17079 Helicobacte AB1515 H. pylori ur AF332656 Helicobac BD092330 Identific AR714224 Helicobac BD092330 Identific AY714224 Sequence CQ903245 Sequence CQ903245 Sequence CQ903246 Sequence CQ903246 Sequence AF75276 Helicobac CQ903246 Sequence AF752376 Helicobac AF75026 Helicobac AF75026 Helicobac AF79026 Helicobac AC00338 C.jejuni DN AF479026 Helicobac AC01398 C.jejuni Ge AC01398 C.jejuni Ge

Perfect score:

Sequence:

Searched:

Database

OM nucleic

Run on:

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Bacteria; Proteobacteria, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae; Helicobacter.

1 (bases 1 to 2883)
Kusters,J.G. and Cattoli,G.
Helicobacter felis vaccine
Patent: JP 2002155054-A 1 10-DEC-2002;
AKZO NOBEL NV
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PF 16-JUL-2000 JP 2001214711
PR 17-JUL-2000 EP 00202565.8
PI JOHANNES GERARDUS KUSTERS,GIOVANNI CATTOLI
PC
C12N15/09,A61K39/106,A61K39/118,A61K39/112,A61K39/175, PC
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C12R1:O1),
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PC A61K39/235,A61K39/39,A61K39/395,A61P1/04,A61P31/04,C12N1/15,
PC C12N1/19,
PC C12N1/21,C12N5/10,C12N9/80,C12Q1/68,G01N33/15,G01N33/50,G01N33/ P
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    /organism="Helicobacter felis"

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10-DEC-2002
16-JUL-2001 BP 2001214711
17-JUL-2000 BP 00202565.8
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er felis" DNA"

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KAYGKRLDIPSGNTLRIGAGGGTRKVQLIPLGGSKKVIGMNGLNNNIADERHKHKALDK
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ERQVLPVKNCRNITKKDFKFNDKTAKITVDPKTFEVFVDGKLCTSKPTSQVPLAQRYT
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Patent: EP 1176192-A 1 30-JAN-2002;
Akzo Nobel N.V. (NL)
Location/Qualifiers
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Helicobacter felis Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;

Helicobacteraceae, Helicobacter.

AX356683.1 GI:18674020 Helicobacter felis Kusters, J.G. and Cattoli, G. Helicobacter felis vaccine

REFERENCE AUTHORS TITLE

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      TCTTCATCAAACGCACCTGCAATCGGTCTTGCGTGTGCGATCGTGTCGCTTTAAAACAAC 2700
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C12N1/19,
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PC A61K39/235,A61K39/39,A61K39/395,A61P1/04,A61P31/04,C12N1/15
PC C12N1/19,
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C12N1/21,C12N5/10,C12N9/80,C12Q1/68,G01N33/15,G01N33/50,G01N33/
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GOIN33/53,GOIN33/566,GOIN33/569//(C12N9/80,C12R1:01),(C12Q1/68,
                                                                   TATGCCCCCTCATTTTTAAAGGAAATTATGCGTAGGTCTTTGGTATTGCTATGTGGGGG
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Helicobacter felis vaccine.
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KAYGKRLDIPSGNTLRIGAGQTRRYVQLIPLGSKKVIGMNGLVNNIADERHKHALDK
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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Helicobacter felis vaccine
Patent: EP 1176192-A 13 30-JAN-2002,
Akzo Nobel N.V. (NL)
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CACACCCCACTTCCTCTCCACAATTCCCTACCGCTCTAGCCAATGGCGTTACAACA 1200
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KAYGKRLDIPSGNTLRIGAGGTRKVQLIPLGGSKKVIGMNGLNNNIADERHKHKALDK
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Helicobacter felis
Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.
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                   CTGCACCTCTAAACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTTCTAGGC
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Pred. No. 0;
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Helicobacter felis vaccine
Patent: EP 1176192-A 4 30-JAN-2002;
Akzo Nobel N.V. (NL)
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Sequence 4 from Patent EP1176192.
AX356686 1 GI:18674023
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Helicobacter felis
Helicobacter felis
Bacterais, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
Helicobacteraceae, Helicobacter.

(bases 1 to 2407)
Kusters, J.G. and Cattoli, G.
Helicobacter felis vaccine
Patent: JP 2002135054-A 4 10-DEC-2002;
                                                                                  2400
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        CAAGACGGCGCATATCACTGTCGATCCTAAAACCTTCGAGGTCTTTGTAGATGGCAAACT 2340
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PC A61K39/235, A61K39/39, A61K39/395, A61P1/04, A61P31/04, C12N1/15,
PC C12N1/19,
PC
C12N1/21, C12N5/10, C12N9/80, C12Q1/68, G01N33/15, G01N33/50, G01N33/P
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G01N33/53,G01N33/566,G01N33/569//(C12N9/80,C12R1:01),(C12Q1/68,
                                            GTGAAACTCACACCCAAAGAGAAAAGTTCTTGTTATATTATGCGGGCGAAGTGGCT
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Pred. No. 0;
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Solution/Qualifiers

1. 2407

/organism="Helicobacter felis"

/mol_type="genomic DNA"

/db_xref="taxon:214"
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PC C12N15/00,C12N5/00,A61K37/02
CC Helicobacter felis vaccine
FH Key Location/Qual
FT CDS (2). (682)
FT CDS (693). (2399
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Helicobacter felis vaccine.
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JP 2002355054-A/4.
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93.6%;
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BD185305
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GGMVVFSEMGDSNASVPTQPVYTREMFGHHGKAKFPTSITTVSKVAYENGVKEKLGL
ERKVLPVKNCRNITKKOPFKFNNKTAHITVDPKTFEVFVDGKLCTSKPASEVPLAQRYT
FF"
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DeargekktyaelmeechHplkkobevmegygnmypdl.gyeatppdgtkl.yyvnwpiep
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KAYGKRLDIPSGNTLRIGAGQTRKYQLIPLGGSKKVIGMNGLVNNIADERHKHKALEK
                                                                                                                                                                                                                                                                 Helicobacter felis
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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/note="unnamed protein product"
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0; Mismatches
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Helicobacter fells vaccine
Patent: EP 1176192-A 10 30-JAN-2002;
Akzo Nobel N.V. (N.)
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2. .682
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EP1176192.
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/organism="Helicobacter
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Sequence 10 from Patent
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/transl_table=
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Matches 2251; Conservative
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                   2606 ACAATG
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                                                         AGTGATTCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAAAGAATTTGGTAAGCTTCC
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Helicobacter felis
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Kusters,J.G. and Cattoli,G.
Helicobacter felis vaccine
Patent: JP 2002355054-A 3 10-DEC-2002;
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C12R1:01),
PC C12N15/00,C12N5/00,A61K37/02
CC Helicobacter fells vaccine
FH Key
FT CDS (3). (681).
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/db_xref="taxon:214"
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(694). (683)
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Location/Qualifiers
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JP 2002355054-A/3
10-DEC-2002
16-UU-2001 JP 2001214711
17-JUL-2000 EP 00202565.8
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Helicobacter felis vaccine.
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Location/Qualifiers
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AX356689
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ORGANISM
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Epsilonproteobacteria; Campylobacterales;

Helicobacter felis Helicobacter felis Bacteria, Proteobacteria, Epsilor Helicobacteraceae, Helicobacter.

Kusters, J.G. and Cattoli, G. Helicobacter felis vaccine

AUTHORS TITLE REFERENCE

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Pred. No. 0;
); Mismatches 145;
                                                   3. [683
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AF330621 B406 bp DNA linear BCT 13-MAY-2003 Helicobacter bizzozeronii tRNA ribosyltransferase gene, partial cds; GidB, complete cds; urease gene cluster, complete sequence and
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Zhu,J. and Chang,Y.F.
Direct Submission

Submitted (21-DEC-2000) Population Medicine and Diagnostic Science,
College of Veterinary Medicine, Cornell University, Tower Road,
Ithaca, NY 14853, USA
Location/Qualifiers
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Helicobacter bizzozeronii
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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Zhu,J., Teng,C.H., Chang,C.F., Chang,C.D., Simpson,K.W., Wei,C.,
McDonough,P., McDonough,S. and Chang,Y.F.
Cloning and characterization of a Helicobacter bizzozeronii urease
                                                                                                                                                                         CGCCGACTTGGTGGTGTGGAATCCTGCCTTTTTTGGCGTGAAACCTAAGATTGTGATTAA
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                                                                                                      TITACAATTITCTCAAAGCCGTATCCGCCCCGGATCTATTGCCGCTGAGGATGTGCTCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1646 AGTCAATGAGGCAGGTTATGTAGATGACACCCTAAATGCAATGAACGGGCGCGCCCATCCA 1705
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 AAAGCCTATGGCAAACGCCTAGATATTCCCTCTGGCAACACGCTACGCATTGGGGCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2328 GAAGGAGITITAGGATGAAATIAACCCCTAAAGAGCTGGACAAGCTCATGTTGCATTATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AAAAGTTAATAAAAAGTAACGAAATTAGGACTATAATCCCATTGCCTTTAAAATTTAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAGGAGTAATAGGTGAAACTCACACCCAAAGAGCAAGAAAAGTTCTTGTTATTATGC
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Pred. No. 1.7e-226;
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LF"
               03-MAY-1995
                                                                                                 Candidatus Helicobacter heilmannii
Candidatus Helicobacter heilmannii
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                1 (bases 1 to 264)
Solnick,J.V., O'Rourke,J., Lee,A. and Tompkins, b.S.
Solnick,J.V., O'Rourke,J., Lee,A. and Tompkins, b.S.
Solnick,J.V., O'Rourke,J., Lee,A. and Tompkins, b.S.
Indect. analysis of urease genes from a newly identified uncultured species of Helicobacter Infect. Immun. 62 (5), 1631-1638 (1994)
8168924
O'M May 3, 1995 this sequence version replaced gi:529422.
Original source text: Helicobacter heilmannii (individual_i) DNA.
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              BCT
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              DNA linear complete cds's.
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Pred. No. 6.8e-217;
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Best Local Similarity 66.4%;
Matches 1709; Conservative
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Submitted (12-JNA-1999) Astra Research Center Boston, 128 Sidney Street, Cambridge, MA 02139, USA
Address all correspondence to: hp@arcb.us.astra.com or Richard A. Alm, Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Lo-See L. Ling, Donald T. Moir, Douglas R. Smith, Braydon C. Guild, Gilles Carmel, Anthony Caruso, Debra M. Mills, Rene Gibson, and Gerald F. Vovis are with Genome Therapeutics Corporation, 100 Beaver Street, Waltham, MA, 02453. Qin Jiang and Diane B. Taylor are with the University of Alberta Department of Medical Microbiology and Immunology, Edmonton, Alberta Canada, T6G 2H7 and the Canadian Bacterial Diseases Network. All other authors are with Astra Research Center Boston, 128 Sidney Street, Cambridge, MA, 02139. Putative identifications, sequence alignments, and name and sequence search capabiblity are available at ARRES World Wide Web Site. (URL)
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Helicobacter pylori, strain J99 section 7 of 132 of the complete
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1 (Bases I to 12037)

3 Man, R. A., Ling, L.S., Moir, D.T., King, B.L., Brown, B.D., Doig, P.C., Smith, D.R., Noonan, B., Guild, B.C., deJonge, B.L., Carmel, G., Tummino, P.J., Carmel, G., Uria Nickelsen, M., Mills, D.M., Ives, C., Vovis, G.F. and Trust, T.J.
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Nature 397 (6715), 176-180 (1999)
2405 CGTCTCTAAGTGGCTTATGAAAACGGCATTAAACACGAGTTGGGCTTGCAAAGAGTTGT
                                                                                 2432 TCTACCGGTCAAAAACTGCCGTAACATCACCAAGAAAGACTTCAAGTTCAACGACAAAAC
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King, B.L., Alm, R.A. and Trust, T.J.
Direct Submission
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complement(143..1852)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCTCTAAACATCGCTGACAATACGATGTGCAAGTGGCGATCCACACCGACACCTTGAA 1687
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                                                                                                                                                                                                                     TCCGGGCAAATGGAACTTGCACCGCATGTTGCGCGCAGCAGAAGAGTATTCTATGAATGT 1471
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                                                                                                                                                                                                                          'note="similar to H. pylori 26695 gene HP0077"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGDMNDDMGGDMGDMGDMGGDMGN."
                                                                                                                      /note="synonym: jhp0072"
5226. 6284
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                                                                                                                                                                                          GAGGGHAPDIIKVAGEHNILPASTNPTIPFTVNTEAEHMDMLMVCHHLDKSIKEDVQF
BADSRIRPQTTAAEDTLHDMGIFSITSSBOSQAMERVGBVITRTWOTADRIKKEPGRELKE
EKGDNUNFRIKRYLSKTIKNPLAIAGISEVVGSVEVGRVADIVLMSPAFPGVKDMII
KGGPIALSQMGDANASIPTPQPVYYREMFAHHGKAKYDANITFVSQAAYDKGIKEELG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FGGGKTLREGMSQSNNPSKEELDLIITNALIVDYTGIYKADIGIKDGKIAGIGKGCNK
MODGVKNNISVGPATFALAGEGLIYTNAGIDTHIHFISPQQIPTAFASGYTTMÄGGG
TGPADGTINYTIIFPERNIKWMLRALEEYSMALGFLAKGNASNDASLADDIEGAGAIGF
KIHEDMGTTPSAINHALDVADKYDVQVAIHTDTLNEAGCVEDTWAAIAGRTHHTFHTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGKLVPGELFLKNETTTINEGKKAVSVKVKNVGDRPVQIGSHFHFFEVNRCLDFDREK
TFGKRLDIASGTAVRFEPGEEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRA
KERGFHGAKSDDNYVKTIKE"
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GKDTRKSGYMVENALVSALTSIGYNVIQIGPMPTPAIAFLTEDMRCDAGIMISASHNP
FEDNGIKFFNSYGYKLKEBEERAIEEIFHDEELLHSSYKVGESVGSAKRIDDVIGRYI
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SDYAKTGDGLVCALQVSALVLESKLVSSIALNPFELYPQSLVNLNIQKKPPLESLKGY
SALLKELDQLEIRHLIRYSGTENKLRILLEAKDEKLLESKMQELKEFFEGQLC"
                                                                                                                                                                                                                                                                                                                          LERQVLPVKNCRNI TKKDMQFNDTTAH I EVNPETYHVFVDGKEVTSKPANKVSLAQL F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKLTPKELDKLMLHYAGELARKRKEKGIKLNYVEAVALISAHIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EEARAGKKTAAELMQEGRTLLKPDDVMDGVASMIHEVGI EAMFPDGTKLVTVHTPI EA
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/transl_table=1
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Query Match 37.8%; Score 1090.8; DB 1; Length 12037; Best Local Similarity 65.3%; Pred. No. 1.4e-207; Matches 1681; Conservative 1; Mismatches 853; Indels 39; Gaps 4;	67 TAATRCTATTATTAATTTTTTTAATAATTACTT-ATTATCATATAATAATATTACT 125	2712 TAATACTAATTCATTTTAAATAATTAGTTAATAAATAACGCTTCTGTTAATCTTAGTAAA 2653	126	2652 TCAAAAGATIGCTACAATTACTCCAACCTIGATIGCGTIAIGTCTTCAAGGAAAAAACAC 2593	186	2592 TTTAAGAATAGGAGAATGAGATGAACTCACCCCAAAGGGTTAGATAAGTTGATGCTCC 2533	246 ATTATGCGGGCGAAGTGGCTAGAAAGCGCAAAGCAGAGGCTTAAAGCTCAACCAGCG	2532	306 AAGCCATTGCTTACATTAGTGCCCATATTATGGACGAGCGCCGTGGAAAAAAACG	2472 AAGCGGTAGCTTTGATTAGTGCCCATATTATGGAAGAAGCGAGAGCTGGTAAAAAGACTG	366 TIGCCCAGCTTATGCAAGAGTGCATGCATCCACTTTTGAAAAAAAA	COMPANY TO THE CONTRACT OF THE PROPERTY OF THE	2352 TGGCAAGATCCAAGAAGTGGAGATCTAGAAGCCACCTTTCCTGATGGTACGTAC	4.8.6. 中国を行行に行るを行行といっているようにある。 はいまん こうしゅんけい はんかい こうかい かんけん おおかけい かんけん かんかん かんかん かんかん かんかん かんかん かんかん か	2292 TAACCGTGCATACCCTATTGAGGCTAATGGTAAATTGGTTCCTGGTGAGTTGTTCT	546	2235 TAAAAATGAAGACATCACTATCAACGAAGGCAAAAAAGCCGTTAGCGTGAAGTTAAAA 2176	606 ATGAAGGCCTAAATCCTTGCATGTGGGTAGCCATTTCCACTTCTTTGAAGTAACTAAC	2175	999	2115	726 CGCTACGCATTGGGGCAGGACAAACCCGCAAAGTGCAGTTGATTCCTCTTGGTGGCAGTA 785	2055 CGGTAAGGTTTGAGCCTGGCGAAGAAAATCCGTAGAATTGATTG	786 AAAAAGTGATTGGCATGAACGGGCTTGTGAATAACATCGCGGATGAACGCCATAAACATA	1995 GAAGAATCTTTGGATTTAACGCATTGGTTGATAGGCAAGCAGGCAACGAAAGAAA	846 AAGCGCTTGACAAAGCGAAATCTCACGGATTT	1935 TTGCTTTACACAGAGCTAAAGAGCGTGGTTTTCATGGTGCTAAAAAGCGATGACAACTATG	878ATCAAGTAAGGAGACTCCCATGAAAATGAAAAAACAAGAATATGTAAATACCT	1875 TAAAAACAATTAAGGAGTAAGAAATGAAAAGATTAGCAGAAAAGAATATGTTTCTATGT 1816	931 ACGGACCCACCAAAGGCGATAAAGTGCGCTTAAGGAGATACCGATCTTTGGGCAGAAGTAG 99	1815 ATGGCCCTACCACAGGCGATAAAGTGAGATTGGGCGATACAGATTTGATCGCTGAAGTAG 1756	991 AACATGACTATACCACCTATGGCGAAGAACTTAAATTTGGCGGGGTAAAACTATCCGTG	1051
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2190 CTCCGGGCAAATGGAACTTGCACCGCATGTTGCGCGCAGAAGAGATTTCTATGAATG 1470 1830 2010 2070 TCCATGGCATTGGCAAGGCAGGAAACAAGGACATGCAAGATGGCGTAAGCCCTCATATGG 1230 GCGTGGGTCCTGCTACTGAAGCGCTAGCTGGTGAAGGCTTAATCGTAACGGCTGGTGGTA 1456 TIGACACACACATCCACTTCATTTCACCCCAACAAATCCCTACAGGGTTTTTGCAAGGGGTG 1396 1275 TAGGTTTCTTAGCTAAAGGTAACGCTTCTAACGACGCGAGCTTAGCGGATCAAATTGAAG 1216 1831 AACACTTAGACATGCTCATGACATGCCACCTAGACAAACGCATCCGCGAGGATTTAC 1890 AATITICICAAAGCCGIAICCGCCCCCGGCICIAICGCGGCIGAAGAIGIGCICCAIGAIA 1950 1155 ATGCGTTAGACGTTGCGGACAATACGATGTGCAAGTCGCTATCCACAGACACTTTGA 975 ACAACATCCTACCGGTTCCACTAACCCCACTATCCCTTTCACTGTGAATACAGAAGCCG 795 resesarrrrereaarcaceaerrereaerrereaedeareseresesereaaerra TCACTAGGACTTGGCAAACAGCTGACAAAAACAAAAAGAATTTGGCCGCTTGAAAGAAG ATGGCAAAGATAACGATAATTTCCGCATTAAGCGCTACATCTCCCAAATACACTATCAACC TCGTGGGGTGTGGGCACAGAAGCACTAGCAGGGAAGGTATGATTATTACCGCTGGGGGAA TTACAACCATGTTTGGAGGGGGCACACAGGTCCTGTAGATGGCACGAATGCGACTACTATCA 1591 ACTGCTTGAGCGTGGCAGATGCAATACGATGTGCCAAGTTTGTATCCACACCGATACAGTCA 1095 ATGAAGCCGGTTGCGTGGAAGACACTATGGCAGCTATTGCCGGACGCACTATGCACTT 1711 ACCACATTGAGGGGGGGGGGGGGACACTCACCTGATGTTATCACCATGGCAGGCGAGC 1771 TCAATATTCTACCCTCCTCCACCACCACTATTCCCTATACCATTAATACGGTTGCAG TGGGTGTGATCGCGATGACAAGCTCGCAATCGCAATGGGGCGTGCAGGCGAAGTGA 2011 TTCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAAGAATTTGGTAAGCTTCCTGAAG CITTAAICGIGGAITACACCGGIAITIATAAAGGGGATAITGGIAITAAAGACGGCAAAA CGATGATTATCGACTACACCGGGATTTACAAAGCCGACATTGGGATTAAAAACGGCAAAA 915 1891 1951 1231 1455 1395 1335 1215 1111 1515 1291 1351 1411 1471 855

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GKUTRKSGYMVENALVSALTSIGYNVIQIGPMFTPALAFLTEDMRCDAGIMISASHNP
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GALHPNQLSQEVKKYRADLGFAFDGDADRLVVVDNLGNIVHGFNLGVLGVVGVSKNA
LSSQAVATNMSNINALKEYLKSODELKHGTAGDKFVSECMQLIKANFGGEGSGHIIF
SDYAKTGDGLVCALQVSALVLESKQVSSVALNPFELYPQSLVNLAVQKKPLESLKGY
SALLKELDKLEIRHLIRYSGTENKLRILLEAKDEKLLESKMQELKEFFEGHLC"

4796. . 5065

/ Gene="HP0076"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / LTAIN LALLONS IN STARKLASTILKRYDELTALLSSAEVVSDIKKLTELSKEGSSI
BEISTASKEYLSVLENIKENKELLEDKELSELAKEELKILETOKSDLETAIKOLLIPK
DPNDDKNIYLELRAGTOGDEAGIFVGDLERAYCRYADLKKWKYEIVSSSENSYGGYKE
ITALKGKGVYSRLKREGTRVQRYNETESGGRIHTSAITVAIMPEVDDVEVSINFS
DLKIEVFRAGGHGGCVAGTYDSAVRITHLPTNISVSWODEKSCHKNKOKALKILKARL
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PID:968930 GB:U00096 percent identity: 52.87; identified
by sequence similarity; putative"
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41.38; identified by sequence similarity; putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="similar to GB:AE000511 PID:2313160 percent identity: 100.00; identified by sequence similarity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_table=11
product="peptide chain release factor RF-1 (prfA)"
protuct="peptide chain release factor RF-1 (prfA)"
protein id="AbD07148.1"
|db_xref="G1:2313158"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        predicted coding region HP0078
/note="similar to GB:M60398 SP:P25177 PID:149008 GB:AE000511 PID:2313156 percent identity: 100.00; identified by sequence similarity; putative".codon start=1 /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="outer membrane protein (omp3)"
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/db xref="G1:2313160"
                                                                                                           /product="urease protein
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/db_xref="G1:2313156"
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6658. .6915
/gene="HP0078"
6658. .6915
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/transl_table=11
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/gene="HP0079"
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/gene="HP0077"
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/gene="HP0077"
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/gene="HP0078"
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/transl_table=1
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/transl_table=
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ALQQAESKLINTDQQTLINTALQDQTKTPTPSTPPTKEEPRHTASSGTPPPABESPFAKKD
ETSGTPBSAGSSOVASQLTKDTTWYNLLKSVSVAMNTTLSQVETWSQDTATTGNLINS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 TTATATTATGCGGGCGAAGTGGCTAGAAAGCGCAAAGCAGAGGGCTTAAAAGCTCAACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                               794; Indels
                                                                                                                                                                                                                                                                                                                                                                                            Score 1081.6; DE
Pred. No. 1e-205;
0; Mismatches 79
                                                                                                                                                                                                                                                                                                                /gene="HP0080"
8959. .10740
                                                                                                                                                                                                                                                                                                                                                                                              37.5%;
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AAAACGGCAAAAATCACCGTCGATCCGAAAACCTTCGAGGTCTTTGTAGATGGCAAACTC 2546
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                                                                                                                     GAAGAAAAAGGCGATAACGACAACTTCAGGATCAAACGCTACTTGTCTAAATACACCATT
                                                         AACCCCGCTTTGACCCACGGCGTGAGCGAGTATATCGGCTCTGTGGAAGAGAGGCCAAGATC
                                                                                                                                                                      78 ACACTITAAGAATAGGAGAATGAATGAAACTCACCCCAAAAGAGITTAGATAAGTIGATG
                                                                                AACCCAGCGATCGCTCATGGGATTAGCGAGTATGTAGGTTCTGTAGAAGTGGGCAAAGTG
                                                                                                         GCCGACTTGGTGGTGTGGAATCCTGCCTTTTTTGGCGTAAAACCCAAAATCGTGATCAAA
                                                                                                                                                         GCCGGTATGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCCACTCCCCAA
                                                                                                                                                                                                        CCGGTTTATTACCGCGAAATGTTTGGGCATCACGGCAAGGCGAAATTTGACACCAGCATC
                                                                                                                                                                                                                     TTATATTATGCGGGCGAAGTGGCTAGAAAGCGAAAGCAGAGGGCTTAAAGCTCAACCAA
          GAAGATGGCAAAGATAACGATAAATTTCCGCATTAAGCGCTACATCTCCAAATACACTATC
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183 GTAACTTCTAAACCAGCCAATAAAGTGAGCTTGGCGCAACTCTTTAGCATTTTCTAGG
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Multimeric, recombinant urease vaccine
Patent: US 5837240-A 1 17-NOV-1998;
Location/Qualifiers
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Pred. No. 2.4e-204;
); Mismatches 798;
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    2735
/organism="unknown"
/mol_type="unassigned DNA"

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Sequence 1 from patent US 5837240.
AR054309
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Matches 1622;
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AR054309
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FEATURES
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AUTHORS
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ATGTATGGCCCCTACTACAGGCGATAAAGTGAGATTGGGCGATACAGACTTGATCGCTGAA 1744
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                       GTAGAACATGACTATACCACCTATGGCGAAGAACTTAAATTTGGCGCGGGGTAAAACTATC
                                                                       CGTGAGGGTATGGGTCAGAGCAATAGCCCTGATGAAAACACCCTAGATTTAGTCATCACT
                                                                                    AGAGAAGGCATGAGCAATCCAACAACCTAGCAAAGAAGAATTGGATCTAATCATCACT
                                                                                                                       AACGCGATGATTATCGACTACACCGGGATTTACAAAGCCGACATTGGGATTAAAAACGGC
                                                                                                                                  AAAATCCATGGCATTGGCAAGGCAGGAAACAAGGACATGCAAGATGGCGTAAGCCCTCAT
                                                                                                                                                                                              AAAATCGCTGGCATTGGTAAAGGCGGTAACAAGACATGCAAGATGGCGTTAAAAACAAT
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Search completed: November 29, 2005, 04:30:37 Job time : 14066 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		ouerv			SUMMARIES		
No.	Score	Match	Length	DB	ΠD	Description	ion
н	327.4	11.4	958	00	DR637438	DR637438	EST102806
0	324.2	11.2	946	œ	DR637093	DR637093	EST102771
٣	310.2	10.8	1509	4	CNS0ABR8	BX816461	Arabidops
4	309	10.7	872	7	C0122599	CO122599	GR ED04F
'n	306.2	10.6	925	Φ	DR633422	DR633422	EST102404
9	302.2	10.5	748	Φ	CX676965	CX676965	ydd29h04.
7	299.2	10.4	889	Φ	DR637386	DR637386	EST102801
æ	296.4	10.3	796	œ	DR633939	DR633939	EST102456
σ	292	10.1	849	Φ	DR635599	DR635599	EST102622
10	279.6	9.7	166	7	CV195867	CV195867	CGF100344
11	274.2	9.5	986	9	CF826586	CF826586	EST703968
12	273	9.5	784	σ	AZ935182	AZ935182	BJ Ba000
13	262.6	9.1	066	7	C0027797	C0027797	EST806181
14	261.2	9.1	684	7	CN907928	CN907928	030109ABL
15	261	9.1	921	9	CF714848	CF714848	CCAF343TO
16	261	9.1	946	œ	DN809412	DN809412	73954613
17	259.6	9.0	713	7	CK757406	CK757406	atr02-4ms
18	258.2	9.0	689	ထ	DR440006	DR440006	EST149 09
19	255.2	8 6.	781	ω	DR916924	DR916924	EST110846
20	254.8	8.8	863	9	CD375065	CD375065	PTMM00226
21	254.4	8.8	945	Φ	DN808832	DN808832	76945303
22	249.4	8.7	757	ហ	BU027777	BU027777	QHG7L07.y

CA264652 SCQCLB204 CN908312 030109ABL CP708414 CCABR70TR CA236757 SCEQFL505 CV902222 PD019F1 m AQ94016 Drosophil DN810553 76554039 BC887260 EST513111 CF68903 CCADS40TF CN910029 030124ABL CX557362 Ydd35hil. AW618902 EST32088 CF690511 CCAAZ91TR AZ93508 BJ Ba000 BZ572656 mshZ 2738 CF706674 CCARE33TO AZ93571 BJ Ba000 BZ572656 mshZ 2738 CF706674 CCARE33TO AZ93571 BJ Ba000 BZ572566 mshZ 2738 CF706674 CCARE33TO AZ93571 BJ Ba000 BZ572566 mshZ 2738 AZ95571 BJ Ba000 BZ57256 mshZ 2738 AZ95571 BJ Ba000 BZ57256 mshZ 2738	AG939430 Drosophil CF702527 CCAHQB3TF AG941093 Drosophil
CA264652 CN908212 CA28414 CA236757 CV902222 AG810553 BG887260 CY6899903 CN618902 CN851837 CN851837 CN851837 CN851837 CN851837 CN8518300 CN85183008 BZS72656 CFC CFC CFC CFC CFC CFC CFC CFC CFC CFC	AG939430 CF702527 AG941093
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# ALIGNMENTS

RESULT 1 DR637438 LOCUS DEFINITION	DR637438 958 bp mRNA linear EST 11-JUL-2005 EST1028063 FvM Gibberella moniliformis cDNA clone FVMAW64, mRNA
ACCESSION VERSION	sequence. DR637438 DD637438.1 GI:70712272
SOURCE ORGANISM	Gibberella moniliformis Gibberella moniliformis
	Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes; Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
REFERENCE AUTHORS	<pre>1 (bases 1 to 958) Brown,D.W., Cheung,F., Proctor,R.H., Butchko,A.E., Zheng,L, Lee,Y.,</pre>
	Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
TITLE	Analysis of 87,000 expressed sequence tags reveals alternatively
JOURNAL	Spinced include in matciple genes of the ramonism gene creater Unpublished (2005)
COMMENT	Contact: Brown, D.W. USDA/ARS/NCAUR
	1815 N. University St. Peoria, IL 61604, USA Tel: 309 681 6230
	Fax: 309 681 6689
	Email: browndw@ncaur.usda.gov
	Tick sequence name: Fvwwwsin
0000000	Seq primer: AAT TAA CCC TCA CTA AAG GG.
SOUTCE	1958
	/organism="Gibberella moniliformis"
	/mol_type="mRNA"
	/BCIGIN="MS125" /Ab <**of="t=<">*of="t=<"t">*of="t=<"t">*of="t=<"t">*of="t=<"t">*of="t
	/clone="FWAW64"
	/tissue type="mycelia"
	/clone lib="FvM"
	/note="Vector: pBlueScript II SK(+) XR; Site_1: EcoRI;
	Site_2: XhoI; anamorph: Fusarium verticillioides. Library
	FvM was prepared from pooled RNA obtained from a 48-hour
	and a /2 hour, liquiq GiAm cuiture trom strain m-size.
	Cultures were vacuum filtered and the mycellar made were
	added to TRIzol Reagent (Invitrogen. Carlabad CA) at
	approximately 1 g mycelia per 10 ml TRIzol. The cDNA was

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directionally ligated into the pBlueScript II SK(+) vector (cDNA Synthesis Kit; Stratagene)."
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Pred. No. 3.5e-70;
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I (bases I to 94).

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Aredra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 97,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005).
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Pred. No. 2.2e-69;
0; Mismatches 378;
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TIGR sequence name: FVMAT95TH
Seq primer: AAT TAA CCC TCA CTA
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Tel: 309 681 6230
Fax: 309 681 6689
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Gibberella moniliformis
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ilarity 59.7%;
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Best Local Similarity
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Castelli

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http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GATGAACATCTTGACATGCTGATGGTTTGCCATCACCTTGACAAGAACATCCCAGAAGAT 300
The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length librairies construction: Temple G.
Genoscope members carried out sequencing and annotation: Castel V., Aury J.M., Jailno O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA: Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATCACTGCTTGAGCGTGGCAGATGAATACGATGTGCAAGTTTGTATCCACACCGATACA
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Pred. No. 7.7e-66;
0; Mismatches 413;
                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Hormone Treated
/ecotype="Col-0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                   clone="GSLTPGH4ZD08"
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[ bases 1 to 1509]

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome
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         CAACTTGTAGAACAAGTAGAAGCGGGCGCGATTGGTTTTAAATTGCATGAAGACTGGGGGC 1568
                                                                                                                                                                                         1629 TGTATCCACACCGATACAGTCAATGAGGCAGGTTATGTAGATGACACCCTAAATGCAATG 1688
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                                                                                                                                            421
                                                                                                                                                                                                                                      422 CTTATTCACACTGACACGCTTAACGAGTCTGGCTTTGTCGAATCTACGATCGCTGCTTTC 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATACCATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATGCCACCACCTAGAC
                                                   GGTCTGCGCGATCAGGTCAATGCTGGTGCTTGTGGCCTTCAAGCTTCATGAGGACTGGGGT
                                                                                                1569 ACAACACCAAGTGCGATCGATCACTGCTTGAGCGTGGCAGATGAATACGATGTGCAAGTT
                                                                                                                                            362 TGCACTCCTGCTGCTATTGACGCTTGTCTCAGTGTCTGTGATGAATTCGATATTCAATGT
                                                                                                                                                                                                                                                                                  AACGGGCGCCCATCCATGCCTACCACATTGAGGGAGGGGGGTGGAGGACACTCACCTGAT
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HTC, GSLT. CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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CNSOABR8
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DEFINITION
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AUTHORS
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925 bp mRNA linear EST 11-JUL-2005 FvM Gibberella moniliformis cDNA clone FVWA534, mRNA
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Gibberella moniliformis
Bukaryota; Pungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
GGGGAAGGTATGATTATTACCGCTGGGGGAATCGATTCACACACCCCACTTCCTTTCTCCA
                                                                                                                                CCTGTAGATGCCACGAATGCGACTACTATCACTCCGGGCAAATGGAACTTGCACGCATG
                             GGAGAAGGATTGATCGTAACTGCAGGGCTATTGACTGTCATGTGCATTTCATATGTCCT
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GR ED04F01 5',
                                                                              CAACCGGTTTATTACCGCGAAATGTTTGGGCATCACGGCGAAGGCGAAATTTGACACCAGC 2363
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicotyledons,
rosids, eurosids II; Malvales, Malvaceae, Malvoideae, Gossypium.
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Kim,H., Yu,Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
Wing,R.A.
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Eb Gossypium raimondii cDNA clone GR
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Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Thes University of Arizona
Tel: 520 626 9595
Fax: 520 621 1259
Email: ruing@genome.arizona.edu
Plate: 04 row: F column: 01.
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/mol_type="mRNA"
/db_xref="taxon:29730"
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CO122599.1 GI:48821286
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/organism="Strongylocentrotus purpuratus"
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Strongylocentrotus purpuratus
Eukarryotentrotus, Echinodermata; Eleutherozoa;
Echinoidea; Buechinoidea; Echinacea; Echinoida;
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Unpublished (2004)
Contact: Dr. James A. Coffman
Washu Sea urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, 1
Tel: 314 286 1800
Fax: 314 286 1810
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/clone_lib="Sea urchin EST Lib1"
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/db_xref="taxon:7668"
/clone="ydd29h04"
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/tissue type="mycelia"
/clone lib="FVMA534"
/clone lib="FVM"
/clone lib="FVM"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site_2: XhoI; anamorph: Fusarium verticillioïdes. Library
FVM was prepared from pooled RNA obtenined from a 48-hour
and a 72 hour, liquid GYAM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
frozen in liquid nitrogen, ground to a powder, and then
added to TRIZOI Reagent (Invitrogen, Carlsbad CA) at
approximately I g mycelia per 10 ml TRIZOI. The CDNA was
directionally ligated into the pBlueScript II SK(+) XR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1312 TITCTCCACAACAATTCCCTACCGCTCTAGCCAATGGCGTTACAACCATGTTTGGAGGCG 1371
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                                  Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L. Lee, N. Utterback, T., Smith, S., Feldhlyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster Unpublished (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector (cDNA Synthesis Kit; Stratagene).
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                                                                                                                                                                                                                                                                                                                                           61604,
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                                                                                                                                                                                                                                                                                                                                 1815 N. University St., Peoria, IL 61
Tel: 309 681 6230
Fax: 309 681 6689
Email: browndw@ncaur.usda.gov
TIGR sequence name: FVMA534TH
Seq primer: AAT TAA CCC TCA CTA AAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           xref="taxon:117187"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="m3125"
                                                                                                                                                                                                                                        Contact: Brown, D.W.
USDA/ARS/NCAUR
          (bases 1 to 925)
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Matches 54
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1 (bases 1 to 748)
Coffman, J.A., Robertson, A.J., Clifton, S., Pape, D., Hillier, L.,
Martin, J., Wylie, T., Dante, M., Meyer, R., Theising, B., Bowers, Y.,
Gibbons, M., Ronko, I., Tsagareishvili, R., Ritter, E., Kennedy, S. and
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490 ccaacccracaagaccarrcacacgaaraccrcrcgargaggarcrcgarargcrrargg
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                                                                                     1852 CATGCCACCACCTAGACAAACGCATCCGCGAGGATTTACAATTTTCTCAAAGCCGTATCC
                                                                                                                                                                                                                                      GCCCCGGCTCTATCGCGGCTGAAGATGTGCTCCATGATATGGGTGTGATCGCGATGACAA
                                                                                                                                                                                                                                                                                                                       610 GTGCTGAAACCATTGCTGCTGAGGATGTATTACACGACAAAGGCGCTATCAGCATGATGA
                                                                                                                                                                                                                                                                                                                                                                                                    GCTCGGATTCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTCCTCGAACTTGGCAGACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  548
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Site_2: Smal; Arrayed normalized library of full-length
cDNAs representing blastula stage transcriptome of the
urchin Strongylocentrotus purpuratus, cloned into the
vector pCMYSport6.1 (Invitrogen)"
                                                                                                                                                                                                                                                                                                                                                                                                                        CCTACCACATTGAGGGAGGGGTGGAGGACACTCACCTGATGTTATCACCATGGCAGGCG
                                                                                                                                                                                                                                                                                                CAGAACACTTAGACATGCTCATGACATGCCACCTAGACAAACGCATCCGCGAGGATT
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                                                                                                          Gaps
                                                                                                          ö
                                                                              Length 748,
                                                                                                          Indels
                                                                              Score 302.2; DB 8;
Pred. No. 6.3e-64;
0; Mismatches 273;
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Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes; 1 Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella. 1 (base) 1 to 889)

Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L. Lee, Muterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Mhitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster
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TIGR sequence name: FVWAV95TH
Seq primer: AAT TAA CCC TCA CTA AAG
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Contact: Brown, D.W.
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1815 N. University
Tel: 309 681 6230
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Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST 11-JUL-2005
FVMA846, mRNA
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/clone lib="FvM"
/note="Vector: pBlueScript II SK(+) XR; Site 1: EcoRI;
Site 2: XhOI; anamorph: Fusarium verticillioIdes. Library
FvM was prepared from pooled RNA obtained from a 48-hour
and a 72 hour, liquid GYAM culture from strain M-3125.
Cultures were vacuum filtered and the mycelial mats were
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
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FvM Gibberella moniliformis cDNA clone
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Location/Qualifiers
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Tel: 309 681 6230
Fax: 309 681 6689
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frozen in liquid nitrogen, ground to a powder, and then added to TRIzol Reagent (Invitrogen, Carlebad CA) at approximately 1 g mycelia per 10 ml TRIzol. The CDNA was directionally ligated into the pBlueScript II SK(+) XR vector (CDNA Synthesis Kit; Stratagene)."
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Contract: Abhaya Dandekar, PhD
CAES Genome Facility
UC Davis, Department of Pomology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 752 7784
Fax: 530 752 8502
Email: andandekar@ucdavis.edu
Seq primer: WSCF-TCCGAGGACGAGC.
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                                                                                                              I (bases 1 to 849)
Brown, D.W., Cheung, F., Proctor, R.H., Butchko, A.E., Zheng, L., Lee, Y., Utterback, T., Smith, S., Feldblyum, T., Glenn, A.E., Plattner, R.D., Kendra, D.F., Town, C.D. and Whitelaw, C.A.
Analysis of 87,000 expressed sequence tags reveals alternatively spliced introns in multiple genes of the fumonisin gene cluster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCCCAAGTGCTGGAACGAACTACTTGTACGCGCTGGTGCTCATTACATGCGTCAA 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 AGTICTCCTGAGGGTCTGCGCGATCAGGTCAATGCTGGTGCTTGTGGCCCTCAAGCTTCAT
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                                                                                    Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Hypocreomycetidae, Hypocreales, Nectriaceae, Gibberella.
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                                                                                                                                                                                                                                                                                          61604, USA
                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Gibberella moniliformis"
                                                                                                                                                                                                                                                                  USDA

1815 N. University St., Peoria, IL 61604, U

Tel: 309 681 620

Fax: 309 681 6689

Email: browndw@ncaur.usda.gov

TIGR sequence name: FVMAJ6TH

Seq primer: AAT TAA CCC TCA CTA AAG GG.
                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="m3125"
/db_xref="taxon:117187"
                                                                  Gibberella moniliformis
                 GI:70710433
                                                                                                                                                                                                                    Unpublished (2005)
Contact: Brown, D.W.
USDA/ARS/NCAUR
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/clone lib="Seed coat from mid-season walnut embryos collected Aug 1" /note="Organ: Seed coat; Vector: pTriplEx2; Site_1: SfilA; Site_2: SfilB; Walnut nut samples were harvested_from Tulare trees growing in the 'Stuke Block' in the Wolfskill experimental orchard located in Winters, California (USA).
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                                                                                                                                                                                                                                                            1797 CCCACTATTCCCTATACCATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATGC 1856
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1 (bases I to 766)
Muir,R., Baek,J., Leslie,A., Cook,D. and Dandekar,A.
Analysis of genes expressed in walnut seed coat tissue
363 ATCGCTGCTTTCAAGAACCGCACAATTCATACTTATCACACAGAGGGTGCAGGAGGTGCAGGAGGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    723 AAAATAAGGTGCAGAGGGGTTGGTTGCCGGAGGATGAGGGCCACAGGGGCTGATAATGCG 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1977 GATTCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTCCTCGAACTTGGCAGACTGCGGAT
                                                                                                                                                                                       423 CATGCTCCGGATATCATCTCCGTGGTAGAGCATCAAAATGTTCTGCCATCATCGACCAAC
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                                                                                                                                                                                                                                                                                                                                         483 CCTACAAGACCATTCACACCCAATACTCTCGATGAGCATCTCGATATGCTTATGGTCTGC
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Samples were harvested on August 1, 2001 between 8 and 10 am. Samples were then dissected the same day. Seed coat (pellicle) tissue was separated from embryos and frozen immediately in liquid nitrogen and stored at -80C. A gram of sample was removed and ground to a fine powder in liquid nitrogen. Total RNA was extracted using the hot borate procedure. Poly A+ RNA was obtained using the Poly(A) Purist kit (Ambion). The cDNA Library was constructed using the SMART cDNA library was constructed using the SMART cDNA library was fooly in Paramary library was en masse evicted and plasmid DNA containing the cDNA library was isolated from the resultant bacterial population. Plasmid DNA was then transformed into ultra competent E coli cells (KI10 Gold; Stratagene). Transformants were plated out on Q-trays (2000 CEU/tray), picked using a Qbot and archived in 384
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Pred. No. 2.8e-58;
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Matches 462; Conservative
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Eukaryota; Pungi; Ascomycota; Pezizomycotina; Eurotiomycetes; Onygenales; mitosporic Onygenales; Coccidioides.

1 (bases 1 to 986)

25 Gardner, M. J. and Cole, G. T.
Analysis of gene expression in Coccidioides posadasii mycelia and spherules via expressed sequence tags

10 Unpublished (2003)

11 Other ESTS: EST703969

12 Contact: Gardner MJ

13 Fal: 301 838 3519

14 Fal: 301 838 3519

15 Fax: 301 838 2508
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                              CF826586
EST701968 Coccidioides posadasii saprobic phase cDNA library, 2 to 4 kb Coccidioides posadasii cDNA clone CIDB361 3' end, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol type="mRNA"
/strain="C735"
/db xref="taxon:199306"
/db xref="taxon:199306"
/clone="C1DB361"
/dev stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii saprobic phase CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism≈"Coccidioides posadasii"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: gardner@tigr.org.
Location/Qualifiers
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                                                                                                                                    CF826586.1 GI:45932643
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Gaps

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COO27797 10-JUN-2004 ESTB06181 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3 kb Coccidioides posadasii cDNA clone CIFAM57 3' end, mRNA sequence.
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Coccidioides posadasii
Eukaryota; Fungii Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
1 (bases 1 to 990)
Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
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                                                                                                                                                                        1468 ATGTGGGCTTTTTGGGCAAAGGCAATAGCTCTAGCAAAAAAACAACTTGTAGAACAAGTAG
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                                 Length
                         Score 273; DB 9; Lu
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0; Mismatches 253;
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Other ESTs: EST806182
Contact: Gardner MJ
                             9.5%;
ilarity 64.0%;
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Balloo3020f B. japonicum BAC library Bradyrhizobium japonicum
AZ935182
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Tomkins,J.P., Wood,T.C., Stacey,M.G., Loh,J.T., Judd,A.,
Goicoechea,J.L., Stacey,G., Sadowsky,M.J. and Wing,R.A.
A marker-dense, sequence-ready map of the Bradyrhizobium japonicum
GGATTCTGATAATTTTAGGGTTAAACGGTATATCAGCAAGTACACCATCAACCCTGCCAT 567
                                                                                                                                                                                                                                                                               447
                                                                                                                                                                                                                                                                                                                                                                                                     446 TGTCTCAGCGCAGATGATGCTCCAATGGCTCTATCCCCACAATCGAGCCTATTATTAT 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u> Aargagagricgarccggagagcrargrrgrcgaggcrgacgggaagagrgcaccggrga</u>
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                                                                  GACCCACGCCGTGAGCGAGTATATCGGCTCTGTGGAAGAGGGCAAAGATCGCCGACTTGGT
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Bradyrhizobium japonicum
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Bradyrhizobium.
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/lab_host="B. col!"
/clone llb="B. daponicum BAC library"
/note="Vector: pindigo536; Site_1: HindIII"
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Clemson University
100 Oordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/strain="USDA110"
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Class: BAC ends
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/tissue_type="Cell cultures"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGTGCAGGCGAAGTGATTCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAATTT 2054
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                                                                                                                                                                                         /dev stage="spherules"
/lab host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.5 to 5.3 kb"
/note="Vector: pExpress 1; Site_1: Not I; Site_2: Eco RV;
coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTCTCTCGAGAAGTTGTTCGGACATGGAACACTGCACATAAGAATAAAATGGAACGA
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                                                                                                                                                                                                                                                                                                                                           9.1%; Score 262.6; DB 7; Length 990; 58.8%; Pred. No. 5.2e-54; tive 0; Mismatches 339; Indels 29
                    20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    390 ATCCCCACAATCGAGCCTATTATTATGAGGCCTATGTACGCTCCTCA
                                                                                                              /organism="Coccidioides posadasii"
/mol type="mRNA"
/strain="C735"
The Institute for Genomic Research 9712 Medical Center Drive, Rockville, MD 3712 Hel: 301 838 3519 Fax: 301 838 0208 Email: gardner@tigr.org.
                                                                                                                                                                /db_xref="taxon:199306"
/clone="CIFAM57"
                                                                                                                                                                                                                                                                                                                                                                            525; Conservative
                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 525; Conserv
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030109ABLC001286HT (ABLC) Braeburn cell culture three days after
subculture Malus x domestica cDNA clone ABLC001286, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosida I; Rosales; Rosaceae; Maloideae; Malus.

1 (bases 1 to 684)

Beuning,L., Bowen,J., Crowhurst,R., Gleave,A., Janssen,B., McArtrey,S., Newcomb,R., Ross,G., Snowden,K., Walton,E. and Yauk,Y. Unpublished (2004)
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subculture)"
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295 TACCACCTGAAGAAGCGGATCGAGCCAGTGAAGAATTGTCGGAATATAAGCAAGAGAGAT
                                                            2472 TTCAAGTTCAACGACAAAAACGGCAAAAATCACCGTCGATCCGAAAACCTTCGAGGTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Gleave, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand
Fel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
                                                                                                                                                                                                                                                           GCTGACGGGGAAGAGTGCACCGCTGAGCCAGTGTCAGAGTTGCCTTTAACACA 123
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    . 684
    /organism="Malus x domestica"
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Search completed: November 29, 2005, 07:20:55 Job time : 10217 secs
                  Query Match
Best Local Similarity 55.4%;
Matches 504; Conservative
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                                                                                                                                                                                                                                                                                        2026 AGACTGCGGATAAGAATAAAAAAGAATTTGGTAAGCTTCCTGAAGATGGCAAAGATAACG 2085
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Eukaryota; Fungi; Basidiomycota; Hymenomycetes;
Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="C.neoformans strain JEC21"
/note="Vector: pCMVSport6; Site 1: Not! EcoRV; The full
length, normalized library was prepared from a variety of
conditions using RNA provided by Joseph Heitman and
Jennifer Lodge"
                                                                                                                                                                                                                                                                                                                    483 AAACAGCTGACAAGATGAAATCACAAAGAGGTCGATAGAACCTAGTGGATCCGACAATG 542
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End sequencing of clones from a Full length enriched, normalized
                                                                                                      303 rearestruccearcacerrascaaseacarrecasaasarerascrurrecreaarcaa
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                                                                                                                                            GTATCCGCCCCGGCTCTATCGCGGCTGAAGATGTGCTCCATGATATGGGTGTGATCGCGA
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                                 carcaacgaarcccacacgccrircaccrcaaaracraaargagcarcrigarargc
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/mol_type="mRNA"
/strain="JEC21"
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Unpublished (2003)
Other_ESTS: CCAFACO
Contact: Brendan Loftus
The Institute for Genomic Research (TIGR; www.tigr.org)
9712 Medical Center Drive, Rockville, MD 20850, USA
Fax: 301-838-0208
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Seg primer:
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### AAMS   AAMS   AAMS   AAMS   AAMS   AAMS	Urease subunit polypeptide complex encoding sequence. immunogenic fragment; antibacterial; Vaccine; Helicobacter felis; d	ALIGNMENTS	0 612 21.2 3164 4 AAH54464 Aah54464 Aah54469 2 609.6 21.1 1704 8 ACA25712 B AcA20910	3         630.6         21.9         8729         9         ACD19244         Acc19244           4         630.6         21.9         86248         10         ADC00087         Adc00087           6         630.6         21.9         87563.9         ACD19044         Acd19044           6         627.6         21.8         5966         2         AAV74333           7         625.4         21.7         1719         8         ACA54156         Acca4156           8         617.2         21.4         1701         8         ACA35953         Acca35953	880 30.5 1710 9 AALGOS79 Aa160579 876.8 30.4 1717 8 ABA00817 876.8 30.4 1717 8 ABA00817 Aba00817 855.6 29.7 2385 2 AAVG2460 Aav45080 693.4 24.1 24.0 2 AAV19002 AAV19002 693.4 24.1 4768 3 AAZ22097 Aav292097 660.6 24.0 12439 8 ACA46520 Aca46520 664.4 23.0 10000 2 AAT42063 05 Aca46522 658.6 22.8 1698 8 ACA46520 Aca46520 658.6 22.8 1698 8 ACA46522 Aca6652 653 22.7 1710 10 AB701572 Ad46522 664.8 22.0 85814 13 AD705424 Adt05644	Aa16057 Aaq0432 Aaq0432 Aba0080 Aav1900 Aav29209 Aca4522 Continu Aca4522 Adf0154 Adf0154 Adf0154 Adf0154 Adf01934 Adv1433 Aca3595 Aca3595 Aca3595 Aca3595 Aca3595 Aca2591 Aca2591 Aca291 tide complex" tide complex" tide complex" ubunit polypeptides, tions and in the pre	AAL60579 AAQ04329 AAAV08170 AAV19002 AAV19002 AAV19002 AAV19002 AAV14003 AAV140630 AAV140630 AAV140630 AAV140644 AAV16444 AAV019044 AAV019044 AAV19019044 AAV15489 ACA34156 ACA34156 ACA34156 AAV15489 ACA25712 AAV15489 ACA25712 AAV15489 ACA25712 AAV15489 ACA25712 AAV25712 ACA34156 AAV15489 ACA25712 AAV25712 ACA34156 AAV15489 ACA25712 ACA34156 ACA36168 AC	0.5 171 0.6 4 171 0.7 4 171 0.7 4 171 0.7 5 234 0.7 243 0.7 243 0.7 243 0.7 391 0.7 391 0.8 521 0.9 171 0.9	880 876.8 876.8 855.6 734.6 693.4 693.4 693.4 693.4 693.6 664.4 658.6 630.6 631.8 630.6 631.8 630.6 602.8 630.6 602.8 612 602.8 612 602.8 612 602.8 612 612 603.6 603.4 612 603.6 603.8 612 612 612 612 612 612 612 612 612 612	SEGUX S X EXEX X X X X X X X X X X X X X X X
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The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis. Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an urease subunit polypeptide complex encoding sequence of the invention.	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	RGGRAGATTTTCCARCACTTCAAGCACATATTGATCCTGTGTTGTGGGTGAAATTRCR 60 	acttgitaatrctattattaattttaataattacttattatcatatatat	TTACTTATATTAAAAAAGTTAATAAAAAGTAACGAAATTAGGACTATAATCCCATTGCCTT 180 	Tadaatttaacacaaggagtaataggtgaactcacacccaaagagcaagaaaggtctt 240 	GTTATATTATGCGGGCGAAGTGGCTAGAAACGCGAAAGCAGGGCTTAAAGCTCAACCA 300 	accgaagccattgcttacattagtgcccatattatggacgaagcgcgccgtggaaaaa 360 	AACGGTTGCCCAGGTTATGGAAGAGTGCATGCACTTTTTGAAAAAAGAGGAAGGA	CGGGGTGGGTAATATGGTTCCCGATCTAGGTGTAQAAGCCACCTTTCCTGATGGTACGAA 480 	actigiaactgigaaltggcccatcgaaccagatgagcacttcaaagcgggggaggga	attiggticcartaagacatcgactcaaigcagcaaagaagtaaccgaactigaggt 600 	TACTAATGAAGGGCCTAAATCCTTGCATGTGGGTAGCCATTTCCACTTCTTGAAGCTAA 660 	CAAGGCACTAAAATTCGATGGTGAAAAGCCTATGGCAAAGGCCTAGATATTCCCTCTGG 720 	CAACACGCTACGCATTGGGGCAGGACAAACCCGCAAAGTGCAGTTGATTCCTCTTGGTGG 780 	CAGTAAAAAAGTGATTGGCATGAACGGGCTTGTGAATAACATCGCGGATGAACGCCATAA 840 	acataaagggcttgacaaggggaaatctcagggatttatcaagtaaggagactcccatga 900
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The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis. Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an ureaseXY subunit of the invention.
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ive 0; Mismatches
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                                                                                         UreaseXY subunit encoding sequence #1
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                                                                                                                 TGCCTACCACATTGAGGGAGCGGGTGGAGGACACTCACCTGATGTTATCACCATGGCAGG
                                                                                                                                                               CGAGCTCAATATTCTACCCTCCTCCACCACCCCCCACTATTCCCTATACCATTAATACGGT
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                       CGATCACTGCTTGAGCGTGGCAGATGAATACGATGTGCAAGTTTGTATCCACACCGATAC
                                                                    AGTCAATGAGGCAGGTTATGTAGATGACACCCTAAATGCAATGAACGGGCGCGCCATCCA
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Urease; urease gene cluster; urease structural gene;
urease accessory gene; ureABIEFGH; Helicobacter bizzozeronii infection;
antibacterial; gene; ds.
                  H. bizzozeronii urease gene cluster, ureABIEFGH
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                                                                            Helicobacter bizzozeronii
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SIMPSON K W.
ZHU J.
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The invention relates to an isolated nucleic acid molecule conferring on Helicobacter bizzozeronii an ability to produce urease, where the nucleic acid molecule is a urease gene cluster comprising at least one urease cacessory gene. The nucleic acid molecule is a present one urease accessory gene. The nucleic acid molecule is chosen from ureA, ureB, ureF, ureG, ureH and ureI. The invention also relates to an isolated protein encoded by the nucleic acid, and a vaccine for preventing onset of disease in mammals infected by H. bizzozeronii comprising a nucleic acid and a carrier, and an isolated antibody or its binding portion raised against the nucleic acid. The nucleic acids, proteins and antibodies are useful for vaccinating mammals capinst onset of disease caused by infection of H. bizzozeronii, which involves administering the sequences. The sequences are useful for capinal and antiped, providing a nucleotide sequence as a probe in a nucleic acid involves providing a nucleotide sequence as a probe in a nucleic acid and detecting any reaction which indicates that H. bizzozeronii is present in the sample. This sequence represents the H. bizzozeronii is present in the sample. This sequence represents the H. bizzozeronii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule having urease gene cluster, and conferring on Helicobacter bizzozeronii ability to produce urease, useful as vaccine for preventing disease in mammals infected by H.bizzozeronii.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8407 BP; 2264 A; 1937 C; 1969 G; 2237 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                         Claim 2; SEQ ID NO 1; 40pp; English.
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Matches 1681; Conservative
WPI: 2004-533502/51.
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                                                                                                                                                                                                                                                                                                                        Length 2735;
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Pred. No. 3.5e-231;
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Bhagat H,
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Guirakhoo F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "urease A subunit"
                                                                                                                                                                                                                                                                                                                                                                                    pylori ureA + ureB gene locus in pORV214
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Urease; ureA gene; ureB gene; vaccine;
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"T7 terminator"
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/note= "BL1 primer"
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unidentified bacteriophage; T7
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2693. .2735
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                                              CAAGITCTACCGGTCAAAAACTGCCGTAACATCACCAAGAAAGACTTCAAGITCAAGTTCAACGAC
                                                                                   GCCGACTTGGTGGTGTGGAATCCTGCCTTTTTTGGCGTAAAACCCAAAATCGTGATCAAA
                                                                                                                                         GECGGTATGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCCACTCCCCAA
                             AACCCCGCTTTGACCCACGGCGTGAGCGAGTATATCGGCTCTGTGGAAGAGGGCAAGATC
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/note= "ureA Shine-Dalgarno site'
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/note= "ureB Shine-Dalgarno
766. .2475
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/EC number= "3,5.1.5"
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756. .759
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                                                                                      TAAAACGCGCTAAAAAAAAAAGGTTTTGGGTCTGTAAACTGCGGTTGTGAAGCGACTAAAG
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                                                                                                                                                                                                                                  The sequence encodes urease UreA and UreB proteins, which are components of a novel immunogenic composition capable of inducing protective antibodies against Helicobacter infection. The composition may include the UreA or UreB proteins, a urease associated heat shock protein (AAR74338-39) or the UreI protein (AAR74340). The composition is used to prepare a vaccine for humans or animals, especially against H. pylori and H. felis. Antibodies against the proteins may be used for treating Helicobacter infection, and primers/probes to the DNA sequence may be used for detection of Helicobacter infection. (Updated on 25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445
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                                                                                                                                                Immunogenic composition against Helicobacter infection - also gene
fragment(s) and protein(s) from Helicobacter urease gene cluster and heat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 804; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1062.6; DB 2
Pred. No. 2.3e-228;
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65.5%;
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Matches 1606; Conservative
                               PASTEUR.
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                                                                          Suerbaum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New immunogenic compsn. contg. UreB and HspA antigens of Helicobacter for treatment and prevention of esp. H pylori infection, also new antibodies specific for these antigens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           192 ACAAGGAGTAATAGGTGAAACTCACACCCAAAGAGCAAGAAAAGTTCTTGTTATATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A portion (AAT45680) of plasmid pILL205 (CNCM I-1355) comprises the Helicobacter felis structural urease gene encoding urease subunits A (AAW06729) and B (AAW06730). pILL205 was obtd. by examining the expression of urease activity by H. felis cosmid clones and identification of the H. felis genes required for urease expression welloned in E. coli. The urease gene can be used to design probes for detection of Helicobacter infection, or utilised in the prodn. of recombinant urease subunits for use in novel immunogenic compens. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.9%; Score 1062.6; DB 2; Length 2619; ilarity 65.5%; Pred. No. 2.3e-228; Conservative 0; Mismatches 804; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2619 BP; 772 A; 569 C; 665 G; 613 T; 0 U; 0 Other;
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/standard_name= "URE B"
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                       "urease subunit
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Matches 1606; Conserv
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19-MAY-1995;
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GTGTGATCGCGATGACAAGCTCGGATTCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTC 2013
                                                                                                                                                                                                               CTCGAACTTGGCAGACTGCGGATAAGAATAAAAAGAATTTGGTAAGCTTCCTGAAGATG 2073
                                                                                                                                                                                                                                       2006 GGATCGCGCATGGGATTTCTGACTATGTGGGCTCTGTGGAAGTGGGCAAATACGCCGAAC 2065
                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTGGTGTGGAATCCTGCCTTTTTTGGCGTAAAACCCAAAATCGTGATCAAAGGCGGTA 2253
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                                                           TITCTCAAAGCCGTATCCGCCCCGGCTCTATCGCGGCTGAAGATGTGCTCCATGATATGG 1953
                                                                                                                                                                    1826 GGATCTTTTCTATCACCAGCTCCGACTCTCAGGCTATGGGACGCGTAGGCGAGGTGATCA
                                                                                                                                                                                                                                                                                                              1946 AAGGCGATAACGACATCCGCATCAAACGCTACATCTCTAAATACACCCATCAACCCCG
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                                                                                                                                                                                                                                                                                                                                                                   CTTTGACCCACGGCGTGAGCGAGTATATCGGCTCTGTGGAAGAGGGCCAAGATCGCCGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Urease, UreA, UreB, heat shock protein A, HspA, vaccine, immunogen, antigen; antibody; chronic gastritis; ulcer; pILL205; ss.
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1146   GCCTCANTOTTCCCCATTANTCCATGLAGGCCTATCCACCCCATCCCTAACC   1515     1526   AGCCGCCTTATTCCATCCTAATCCATCCATCCTCCCCCCCC	RESULT 10 AAQ75319 ID AAQ75319 standard; DNA; 2619 BP. XX AC AAQ75319;
8	RESU NAQ7 ID XX AC XX
	1534 GCGCGATTGGTTTTAAATTGCATGAAGACTGGGGCACAAGTGCGATCGAT

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GTATGGGTCAGAGCAATAGCCCCTGATGAAACACCCCTAGATTTAGTCATCACTAACGCGA 1113
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                                                                                                               GCATGATTCATGAAGTGGGGGATTGAAGCTAACTTCCCCGATGGAACCAAGCTTGTAACTA
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                  432 ATATGGTTCCCGATCTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTGTAACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori and Helicobacter felis - used to develop
or detection, treatment and prevention of Helicobacter infection.
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                                                                                                      Urease; ureA gene; ureB gene; immunogen; vaccine; diagnostic;
Helicobacter pylori; heat shock protein; HSP; chaperonin; pILL205;
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Pred. No. 5.4e-228;
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                                                                                                                                                           Helicobacter felis, ATCC 49179
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                                                                       Urease ureA/ureB gene
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19-NOV-1993;
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(ORAV-) ORAVAX INC.
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            GCTTTTTGGGCAAAGGCAATAGCTCTAGCAAAAAACAACTTGTAGAACAAGTAGAAGCGG
                                                            GCTTTTTGGCTAAGGGGAATGTGTCTTACGAACCCTCTTTACGCGATCAGATTGAAGCAC
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The invention relates to inducing an immune response against Helicobacter in a mammal, comprising mucosally administering to the mammal an attenuated Salmonella vector containing a nucleic acid molecule encoding a Helicobacter antigen, and parenterally administering to the mammal a Helicobacter antigen, and parenterally administering to the mammal a Helicobacter antigen. Also included is an attenuated Salmonella vector comprising a nucleic acid molecule encoding a Helicobacter antigen. The Helicobacter antigen is a urease, a urease subunit, or its immunogenic fragment (encoded by the ureA and ureB genes). The mammal is at risk of having but does not have Helicobacter infection or has a Helicobacter infection. The attenuated Salmonella vector further comprises an htrA or nitB promoter. The vector can be used in inducing an immune response against Helicobacter in ammmal. The vector can be used to treat
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The vector and the method can be used to treat Helicobacter infection. The vector and the method can be used to treat Helicobacter induced gastroduodenal diseases, including acute, chronic or atrophic gastritis, peptic ulcer diseases (e.g. gastric or duodenal ulcers), and gastric carcinoma. Attenuated Salmonella vector pHUR3 was constructed expressing UreA and UreB and including an E. coli AmpR gene. The present sequence represents the pHUR3 plasmid. NOTE: pHUR3 is represented by both AEB55112 and AEB55130, the peptides expressed by pHUR3 are shown in the sequence listing to be split between AEB55112 and AEB55130, yet Figure 4 shows all the peptides being expressed by the one
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Helicobacter induced gastroduodenal diseases.
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sequence, therefore all encoded peptides are cross-referenced to
                                                              38;
                           BP; 1389 A; 1090 C; 1146 G; 1199 T; 0 U; 0 Other
                                            Score 1058.6; DB 5; Length Pred. No. 2.2e-227; 0; Mismatches 799; Indels
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Helicobacter induced gastroduodenal diseases.
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Salmonella typhimurium.
Escherichia coli.
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comprising mucosally administering to the mammal an attenuated Salmonella vector containing a nucleic acid molecule encoding a Helicobacter antigen. Also included is an attenuated Salmonella vector comprising a nucleic acid molecule encoding a Helicobacter antigen. Also included is an attenuated Salmonella vector comprising a nucleic acid molecule encoding a Helicobacter antigen. The Helicobacter antigen is a urease subunit, or its immunogenic fragment (encoded by the ureB ganes). The mammal is at risk of having but does not have Helicobacter infection or has a Helicobacter in infection. The vector can be used in inmune response against Helicobacter in a mammal. The vector can be used to treat Helicobacter induced gastroduodenal diseases, including acute, chronic or atrophic gastric orcaciona. Attenuated Salmonella vector pHUR3 was constructed expressing UreA and UreB and including an E. coli AmpR gene. The present sequence represents the PHUR3 plasmid. NOTE: PHUR3 is constructed expressed by putMIR3 are shown in the sequence listing to be split between AEB55112 and AEB55130, the peptides expressed by the one SEQUENCE, therefore all encoded peptides are cross-referenced to both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.7%; Score 1058.6; DB 5; Best Local Similarity 65.7%; Pred. No. 2.2e-227; Matches 1606; Conservative 0; Mismatches 799;
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                                              GCGATGACAAGCTCGGATTCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTCCTCGAACT
                                                               TGGCAGACTGCGGATAAGAATAAAAAGAATTTGGTAAGCTTCCTGAAGATGGCAAAGAT
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64..717
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                                                                                                                                                                                                                                                                                 The DNA is a 2.7 kb TaqI fragment encoding the A and B subunits of H. pylori (previously C. pylori) urease, i.e. the 66 and 31 kb antigens. From the sequence, probes and primers can be designed for the manification (by PCR) of the gene, to produce a prods. common to all H. pylori strains so far tested and which do not occur in other ureases and can therefore be used as a specific indication of the presence of H. pylori. H. pylori (previously C. pylori) is strongly implicated in the pathogenesis of gastritis and duodenal and peptic ulceration in man. The primers/probes can be used for the detection of H. pylori DNA in gastric mucosa, saliva or faecal samples to provide an early diagnosis of infection. See also AAQ12434-Q12486. (Updated on 27-AUG-2003 to correct
                                                                                                                                                                                                       Oligo:nucleotide(s) specific for Heliobacter pylori - used as probes and primers to detect H pylori infection, in diagnosis of gastritis, and duodenal and peptic ulceration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence 2767 BP; 867 A; 550 C; 635 G; 715 T; 0 U; 0 Other;
                                                                                                                                    Kleanthous
                                                                                                                                    BW,
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P-PSDB; AAR12515, AAR13550.
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                                                     19-DEC-1989;
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ATGTATGGCCCTACTACAGGCGATAAAGTGAGATTGGGCGATACAGACTTGATCGCTGAA GTAGAACATGACTATACCACCTATGGCGAAGAACTTAAATTTGGCGGGGGGTAAAACTATC 756

AAAATTGCTTTACACAGAGCTAAAAGAGCGTGGTTTTTCATGGCGCTAAAAGCGATGACAAC

CATAAAGCGCTTGACAAGGCGAAATCTCACGGATTT-------

-----ATCAAGTAAGGAGACTCCCATGAAA--ATGAAAAACAAGAATATGTAAAT
TATGTAAAAACAATTAAGGAGTAAGAAATGAAAATTATGTAAAT
TATGTAAAAACAATTAAGGAGTAAGAAATGAAAAAGATTAGCAGAAAAGAATATGCTTCT
ACCTACGGACCCACCAAAGGCGATAAAGTGCGCTTAGGAGAATACCGATCTTTGGGCAGAA

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bizzozeronii ureB"

/product= "H.

US2004142343-A1

L2-AUG-2003; 2003US-00639273 L6-AUG-2002; 2002US-0404337P

Location/Qualifiers 1. .1710 /\*tag= a

Key

Helicobacter bizzozeronii

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GAGCTCAATATTCTACCCTCCTCCACCACCCCCACTATTCCCTATACCATTAATACGGTT 1826
                                                GCAGAACACTTAGACATGCTCATGACATGCCACCACCTAGACAAACGCATCCGCGAGGAT 1886
                                                                                                                           GCCGAACACATGGACATGCTTATGGTGTGCCACCTTGGATAAAAGCATTAAAGAAGAT 1776
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ACTTACCACACTGAAGGCGCTGGCGGCGGACACGCTCCTGATATTATTAAAGTGGCCGGT 1656
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The invention relates to an isolated nucleic acid molecule conferring on Helicobacter bizzozeronii an ability to produce urease, where the nucleic acid molecule is a urease gene cluster comprising at least one urease structural gene and at least one urease accessory gene. The nucleic acid molecule is chosen from ureb, ureb, ureb, ureb, urec, ured, ured, ured and urel. The invention also relates to an isolated protein encoded by the nucleic bizzozeronii comprising a nucleic acid and a carrier and an isolated antibody or its binding portion raised against the nucleic acid. The nucleic acid, proteins and antibodies are useful for vaccinating mammals against onset of disease caused by infection of H. bizzozeronii, which

involves administering the sequences. The sequences are useful for detecting H. bizzozeronii in a sample of tissue or body fluids which mivolves providing a nucleic acid as an antigen, providing an antibody, or providing a nucleotide sequence as a probe in a nucleic acid hybridisation assay, contacting the sample with the antigen or the probe, and detecting any reaction which indicates that H. bizzozeronii is present in the sample. This sequence represents H. bizzozeronii ureB DNA.

Sequence 1710 BP; 492 A; 436 C; 386 G; 396 T; 0 U; 0 Other;

Novel isolated nucleic acid molecule having urease gene cluster, and conferring on Helicobacter bizzozeronii ability to produce urease, useful as vaccine for preventing disease in mammals infected by H.bizzozeronii.

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Simpson KW,

Chang Y,

CHANG Y. SIMPSON K V

(CHAN/) (SIMP/) (ZHOO)

ZHU J.

WPI; 2004-533502/51.

P-PSDB; ADQ37851

Claim 7; SEQ ID NO 4; 40pp; English.

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Query Match 32.6%; Score 940.8; DB 12; Length 1710; Best Local Similarity 72.0%; Pred. No. 4.8e-201; Matches 1227; Conservative 0; Mismatches 477; Indels 0;
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Urease, urease gene cluster, urease structural gene, urease accessory gene, ureB; Helicobacter bizzozeronii infection; antibacterial; gene; ds.

ADQ37850 standard; DNA; 1710 BP.

07-OCT-2004 (first entry) H. bizzozeronii ureB DNA.

ADQ37850;

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This sequence encodes H. felis urease B. This sequence was used in the method of the invention for raising an immune response in an animal. The method comprises administering to the animal a composition comprising a carrier and an antigen bound to a targeting moiety which binds to a least one receptor present in circulatory vessels in Gut Associated Lymphoid Tissue (GALT). The method is useful for raising an immune response in an animal against antigens from Salmonella, Cholera, Helicobacter pylori, HIV, Candida, P. gingivalis, gut parasites, gut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene; rat; IgG2a; light chain; E. coli; galactosidase; immunogen; immune response; circulatory vessel; Gut Associated Lymphoid Tissue; GALT; immune response; antigen; Salmonella; Cholera; immunity; Helicobacter pylori; HIV; Candida; P. gingivalis; gut; parasite; toxin; hormone; hormone receptor; cancer; ss.
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Sequence 680, App Sequence 258, App Sequence 22026, A Sequence 23023, A Sequence 11552, A Sequence 11582, A Sequence 11613, A Sequence 11613, A Sequence 2068, A Sequence 2068, A Sequence 2069, A Sequence 20619, A Sequence 20619, A Sequence 1254, Ap Sequence 20619, A Sequence 1259, Ap Sequence 1488, A Sequence 1259, Ap Sequence 1488, A Sequence 1488, A Sequence 1488, A Sequence 1559, Ap Sequence 1559, Ap Sequence 17 Appli Sequence 1, Appli Sequence 11793,		Length 2883; Indels 0; Gaps 0; TTGTGGGTGGTAATTRCR 60 TTGTGGGTGGTAAATTRCR 60 TTGTGGGTGGTAAATTRCR 60 ATCATATATAATAATAATATTA 120 ATCATATAATCATTAATTA 120 ACTATAATCCCATTGCCTT 180 AAGAGCAAGAAAAGTTCTT 240 AAGAGCAAGAAAAGTTCTT 240
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	506 GAACCAGATGAGCACTTCAAAGCGGGCAAGTGAAATTTGGTTGG	566 CTCAATGCAGGCAAAGAAGTAACCGAACTTGAGGTTACTAATGAAGGGCCTAAATCCTTG 6	626 CAIGIGGGIAGCCAITICCACTICTIGAAGCIAACAAGGCACIAAAATICGAIGGAA 6 		746 CAAACCGGAAAGIGGAGITGATTCCTCTTGGIGGCAGTAAAAAAGIGATTGGCAIGAAC 8 	806 GGGCTTGTGAATAACATCGCGGATGAACGCCATAAACATAAAGGCCTTGACAAGGGCGAAA 8 	866 TCTCACGGATTTATCAAGTAAGGAGTCCCATGAAAATGAAAAAACAAGAATATGTAAA 9 	926 TACCTACGACCACCAAAGGCGATAAAGTGCGCTTAGGAGATACCGATCTTTGGGCAGA 9 	986 AGTAGAACATGACTATACCACCTATGGCGAAGAACTTAAATTTGGCGCGGGTAAAACTAT 1	1046 CCGTGAGGGTATGGGTCAGAGCAATAGCCCTGATGAAAACACCCTAGATTTAGTCATCAC 1	1106 TAACGCGATGATTATCGACTACACGGGATTTACAAAGCCGACATTGGGATTAAAACGG 1	1166 CAAAATCCATGGCATTGGCAAGGCAGAAACAAGGACATGCAAGATGGCGTAAGCCCTCA 1	1226	1286	1346	1406 TATCACTCCGGGCAAATGGAACTTGCACCGCATGTTGCGCGCAGCAGAAGAGTATTCTAT 1	1466 GAATGTGGGCTTTTTGGCCAAAGGCAATAGCTCTAGCAAAAAAAA	
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	QY 2306 ACCGGTTTATTACCGCGAAATGTTTGGGCATCACGGAAAGGCGAAATTTGACACCAGCAT 2365	OY 2366 CACTTTTGTTTCCAAAGTCGCCTATGAAAATGGCGTGAAAGAAA	OY 2426 CCAAGTTCTACCGGTCAAAAACTGCCGTAACATCACCCAAGAAAGA	OY 2486 CAAAACGGCAAAAATCACCGTCGATCGAAAACCTTCGAGGTCTTTGTAGATGGCAAACT 2545	OY 2546 CTGCACCTCTAAACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTTCTAGGC 2605	Qy 2606 ACAATG 2611       Db 2402 NCAATG 2407	RESULT 5 US-09-904-994B-7	; Sequence 7, Application US/09904994B ; Publication No. US20040005325A1 ; GENERAL INFORMATION: ; APPLICANT: AKZO No. US20040005325A1el N.V.		; NUMBER OF SEQ ID NOS: 21 ; SOFTWARE: PatentIn Ver. 2.1 ; SEQ ID NO 7 ; LENGTH: 2183	; TYPE: DNA ; ORGANISM: Helicobacter felis ; FEATURE: ; NAME/KEY: CDS		US-09-904-994B-7.  Query Match	ACCCAAAGAGGAAAAGTTCTTGTTATATTAGGGGGGAAGTGGCT 26	266 AGAAAGCGCAAAGCGTTAAAGCTCAACCAACCGAAGCGTTACTTAGCTTACTTA	326 GCCCATATTATGGACGAGGCCCGTGGAAAAAAACGTTGCCCAGCTTATGGAAGAG 1.1	123 GCCCAIAITAIGGACGAGGCGCCCCGTGGCAAAAACAACGGTGGCTGCTGAACIIAIGGAAAGAA 386 IGCAIGCACTITITGAAAAAAAAGATGAATGCCCGGGGTGGGTAATAGGTTCCCGAT	Db 183 TGTÄTGCÄCTTTTTGAAAAAGGTGATGAGCCCGGTGTGGGGAATATGGTCCCTGAT 242 Qy 446 CTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAACTTGTAACTGTGAATTGGCCCATC 505

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Score 1184.4; DB 7; Length
Pred. No. 7.3e-260;
0; Mismatches 741; Indels
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                                                                 TYPE: DNA
ORGANISM: Helicobacter bizzozeronii
                                                                                                                   41.1%;
PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 8407
                                                                                                                   Query Match
Best Local Similarity 68.5
Matches 1681; Conservative
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Publication No. US2004014234341
GENERAL INFORMATION
APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Zhu, Jiaqian
APPLICANT: Zhu, Jiaqian
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Shupson, Kenneth W
APPLICANT: Shupson, Kenneth W
APPLICANT: Shupson, Kenneth W
APPLICANT: Shupson, Kenneth W
APPLICANTION: HD DIAGNOSTIC AND TREATMENT METHODS
FILE REFERENCE: 19603/3881
CURRENT APPLICATION NUMBER: 60/404,337
PRIOR APPLICATION NUMBER: 60/404,337
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APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: HE DIAGNOSTIC AND TREATMENT METHODS
FILE REFERENCE: 19603/3881
CURRENT APPLICATION NUMBER: US/10/639,273
CURRENT FILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: 60/404,337
PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
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Publication No. US20040241175A1

GENERAL INFORMATION:
APPLICANT: MCKENZIE, BRENT
APPLICANT: BOYLE, JEFFEREY
APPLICANT: LEW, ANDREW
TITLE REPRENCE: BDWP-002
CURRENT APPLICATION NUMBER: US/10/476,313
CURRENT FILING DATE: 2003-10-24
PRIOR FILING DATE: 2001-05-25
NUMBER: OF SEQ ID NOS: 12
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                                                            Length 1710;
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                                                           30.7%; Score 886.4; DB 7;
70.0%; Pred. No. 5.1e-192;
live 0; Mismatches 511;
        NAME/KEY: misc feature LOCATION: (B) LOCATION 1...1710 SEQUENCE DESCRIPTION: SEQ ID NO: 3849:
                                                                     Best Local Similarity 70.0
Matches 1193; Conservative
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CACTTGGATAAAAGCATTAAAGAAGATGTCCAGTTCGCTGATTCAAGGATCCGCCCTCAA
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangeu
APPLICANT: Masclbeck, Robert
APPLICANT: Masclbeck, Robert
APPLICANT: APPLICANT: Cyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
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APPLICANT: Carr, Grant
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APPLICANT: Yamamoto, Robert
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                                                                                                                           Score 885.8; DB 3;
Pred. No. 7.2e-192;
0; Mismatches 512;
 Windows Version 4.0
                                                                                                                          30.7%;
                                      TYPE: DNA ORGANISM: Helicobacter pylori
                                                                                                                                                     Matches 1193; Conservative
                                                             ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)...(1757)
US-09-895-913A-251
SOFTWARE: FastSEQ for
SEQ ID NO 251
LENGTH: 1815
                                                                                                                          Query Match
Best Local Similarity
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Pred. No. 1.2e-191;
0; Mismatches 512;
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essentia FILE REFERENCE: ELITRA, 034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PAPLICATION NUMBER: 60/191, 078
PRIOR PELING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
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PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-110-23
PRIOR PELICATION NUMBER: 60/242,578
PRIOR PELING DATE: 2000-110-23
PRIOR PELING DATE: 2000-112-27
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PELING DATE: 2001-02-09
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69.8%; Pred. No. 1.5e-190;
cive 0; Mismatches 515;
                                                                                                                                                                                                                                                         APPLICANT: PARK, Hee-Sung
TITLE OF INVENTION: Method for producing a
FILE REPERENCE: YLOPO40518US/PCT
CURRENT APPLICATION NUMBER: US/10/500,447A
CURRENT FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: KR 2001-11712
PRIOR PILING DATE: 2001-11-19
                                                                        2603
                                                                                                          GCGCAACTCTTAGCATTTTCTAG 1710
                                                                        GCCCAGCGCTACACTTTCTTGTAG
                                                                                                                                                                                                    Sequence 5, Application US/10500447A Publication No. US20050150016A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
ENGTH: 1710
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ORGANISM: Helicobacter pylori
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 AACGATGCGAGCTTAGCCGATCAAATTGAAGCCGGTGCGATTGGCTTTAAAATTCACGAA
                                                                         673 GACTGGGGCACCACTCCTTCTGCAATCAATCATGCGTTAGATGTTGCGGACAATACGAT
                                                                                                                                                                                             1680 AATGCAATGAACGGGCGCGCCATCCATGCCTACCACATTGAGGGAGCGGGTGGAGGACAC
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Pred. No. 8.1e-190;
0; Mismatches 517;
                                                                                                                                                                                     APPLICANT: MCKENZIE, BRENT
APPLICANT: BOYLE, JEFFEREY
APPLICANT: BOYLE, JEFFEREY
APPLICANT: LEW, ANDREW
TITLE OF INVENTION: Artigen Targeting
FILE REFERENCE: BDWP-002
CURRENT APPLICATION NUMBER: US/10/476,313
CURRENT APPLICATION NUMBER: PR5241
PRIOR APPLICATION NUMBER: PR5241
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 11
 GCCCAGCGCTACACTTTCTTCTAG 2603
                   Sequence 11, Application US/10476313
Publication No. US20040241175A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.4%;
Best Local Similarity 69.7%;
Matches 1187; Conservative
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ORGANISM: Helicobacter pylori
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US-10-476-313-11
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US-10-476-313-11
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                      CTCAGAGCGGCTGAAGAATATTCTATGAACTTTGGTTTTCTTGGCTAAAGGTAACGCTTCT
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APPLICANT: Kim, Byung-0
APPLICANT: Woung-Hwo
APPLICANT: Park, Myung-Hwan
APPLICANT: Choi, Deok-Joon
APPLICANT: Choi, Deok-Joon
APPLICANT: Choi, Deok-Joon
APPLICANT: Ung, Hyung-Jin
TITLE OF INVENTION: Recombinant Microorganisms Expressing Antigenic Proteins of Heliob
FILE REFERENCE: 0136/06140
CURRENT APPLICATION NUMBER: KR 97-11950
EARLIER APPLICATION NUMBER: KR 97-11950
EARLIER APPLICATION NUMBER: KR 97-11950
EARLIER APPLICATION NUMBER: KR 97-11951
EARLIER APPLICATION NUMBER: KR 97-11951
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Pred. No. 6.8e-185;
0; Mismatches 504;
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                                                     Sequence 1, Application US/09402100
Patent No. US20010019834A1
GENERAL INFORMATION:
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; LOCATION: ()..()
; CTHER INFORMATION: Recombinant
US-09-402-100-1
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ORGANISM: Artificial Sequence
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Best Local Similarity 69.8%;
Matches 1169; Conservative
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APPLICANT: Carr, Grant
APPLICANT: Carr, Grant
APPLICANT: Vamamoto, Robert
APPLICANT: Vanamoto, Robert
APPLICANT: Vanamoto, Robert
APPLICANT: Vanamoto, Robert
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: 00/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,98
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-06
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PRIOR PILING DATE: 2000-10-23
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PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-12-22
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58.6%; Pred. No. 3.4e-157;
ive 0; Mismatches 929;
                                                                                                                                                              Sequence 32950, Application US/10282122A Publication No. US20040029129A1
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
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Best Local Similarity 58.6
Matches 1408; Conservative
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Trawick, John
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1259 ATAACAGCGGGTGCTATAGGTCTTAAAATACATGAAGACTGGGGGGGAACGCCAATGGCA 1318  1584 ATCGATCACTGCTTGAGCGTGGCAGATGATGATACGATGTGCAAGTTTGTATCCACACGAT 1643  13.10 ATTCATACATTACTGATGATGATGATGATGATGATGATGATGATGATGATGAT	Search o
ACGTCAATGAGGCAGGTTTTTATGAATGACACCCTAAATGCAATGAACGGGCGCGCCATCAATGAAAGAGGAATGAAAGAGGGGGCGCAATGAAAGAGAATGAAAGAGATGATTTTTATGAAGAGACAGTAAAAGACCATTGCCGGTCGAGTGATCAAA	
1704 CATGCCTACCACATTGAGGGAGCGGGTGGAGGACACTCACCTGATGTTATCACCATGGCA 1763 	
1764 GGCGAGCTCAATATTCTACCCTCCTCCACCCCCACTATTCCCTATACCATTAATAG 1823 	
1824 GTTGCAGAACACTTAGACATGCTCATGACACCCCCCCACCTAGACAAACGCATCCGCGG 1883 	
1884 GATITACAATTITCTCAAAGCCGTAICCGCCCCGGCTCTAICGCGGCTGAAGAIGTGCTC 1943 	
1944 CATGATATGGGTGTGATCGCGATGACAAGCTTCGCAAGCAA	
2064 CCTGAAGATGGCAAAGATAACGATAATTTCCGCATTAAGCGCTACATCTCCAAATACACT 2123 	
2124 ATCAACCCGGCTTTGACCCACGGGGTGAGGGTATATCGGCTCTGTGGAAGAGGGCAAG 2183 	
2184 ATCGCCGACTIGGTGGTGGAATCCTGCCTTTTTTGGCGTAAAACCCAAAATCGTGATC 2243 	
2244 AAAGGGGGTATGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCACTCC 2303 	
2304 CAACCGGTITATTACCGCGAAATGTTTGGGCATCACGGCAAGGCGAAATTTGACACCAGC 2363 	
2364 ATCACTTTTGTTTCCAAAGTCGCCTATGAAAATGGCGTGAAAGAAA	
2424 CGCCAAGTICTACCGGICAAAAACTGCCGTAACATCACCAAGAAAGACTICAAGTICAAC 2483 2159 AGCTIAATIGGICGTGTGGAGGCTGTCGTCATATCACAAAAGCTICGATGATCACAAT 2218	
2484 GACAAAACGGCAAAAATCACCGTCGATCCGAAAACCTTCGAGGTCTTTGTAGATGGCAAA 2543 2219 AACTATGTTCCTCATATCGAATTAGATCCACAAACTTACATTGTTAAAGGGGATGGTGTA 2278	
2544 CTCTGCACCTCTAAACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTTCTAG 2603 2279 CCACTGGTTTGTGAGCCAGCGACTGAATTACCGATGGCTCAACGCTATTTCTTATTTAA 2338	

Search completed: November 29, 2005, 08:04:19 Job time : 2060 secs

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Sequence 4032, Ap
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU348003
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3853
LENGTH: 3234 cerarracaagarareeecerarraarareeaagracaagricaeaagcaareee TGCAGGGGAAGTGATTCCTCGAACTTGGCAGACTGCGGATAAGAATAAAAAGAATTTGG TGTCGGTGAAGTTGTAACACGTACTTGGCAAGTTGCACACGTATGAAAGAACAACGCGG GGGCAAGATCGCCGACTTGGTGGTGTGGAATCCTGCCTTTTTTGGCGTAAAACCCAAAAT CACTCCCCAACCGGTTTATTACCGCGAAATGTTTGGGCATCACGGCAAGGCGAAATTTGA CACCAGCATCACTTTTGTTTCCAAAGTCGCCTATGAAAATGGCCGTGAAAAAGCTGGG GTTCAACGACAAAACGGCAAAAATCACCGTCGATCCGAAAACCTTCGAGGTCTTTGTAGA AAATAATAATGCTACACCTAAAATAGATGTAGATCCACAAACATATGAGGTATTCGTTGA TGGCAAACTCTGCACCTCTAAACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTT TAAGCTTCCTGAAGATGGCAAAGATAACGATAAATTTCCGCATTAAGCGCTACATCCCAA ATACACTATICAACCCCGCTTTGACCCACGCGTGAGCGAGTATATCGGCTCTGTGGAAGA 2142 gegraaactrecceartractaateregeaaccaeartretrecteceaaccearer CGTGATCAAAGGCGGTATGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCC rcraaaacgaarggricgaccagrragaaararragaaarrraacraaggcagarargaa TYPE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic

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GAIGCCIAITAAIGIAGGAITIACIGGIAAAGGICAAGCIGICAAICAIACIGCACITAI 1550
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                                            Length 3234;
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                                            Score 612; DB 1; L. Pred. No. 5.3e-139; 0; Mismatches 845;
  ; OTHER INFORMATION: nucleic acid sequence US-10-793-626-3853
                                              Query Match 21.2%;
Best Local Similarity 57.4%;
Matches 1211; Conservative
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                                                                                                                                                                                                                                                                                                                                                   APPLICAT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480U2
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR PPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver: 2.1
LENGTH: 1716
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JOTHER INFORMATION: Description of Artificial Sequence: synthetic
JCHER INFORMATION: nucleic acid sequence
US-10-793-626-117
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                                                                                                                                                                                                                                                          Sequence 117, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Matches 1021; Conservative
                                                                                         ATTCTAGG 2638
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                                                                                                                                                           720 ATTGATACTCATGTTCATTTATTAATCCTGAACAAGCAGAGGTCGCATTAGAAAGTGGT
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RESULT 4
US-10-485-517-26

J Sequence 26, Application US/10485517

Publication No. US20050256299A1

GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Biosynexus Incorporated
APPLICANT: Poster, Simon
APPLICANT: Mond, James
TITLE NOF INVENTION: Antigenic Polypeptides
FILE REFERENCE: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
PRIOR FILING DATE: 2002-01-09
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.8%; Score 455; 57.5%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-485-517-26
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Matches 928; Conservative
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Sequence 4032, Application US/10793626 Publication No. US20050255478A1

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2370 CTGCAGTGAGATTTGAACCTGGAGATGAAAAAAAGTACAACTTGTCGAATATTCTGGAC 2429
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                         GTAAAAAGTGATTGGCATGAACGGGCTTGTGAAT
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        APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: 1013480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PAPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAATATGAAAGAAGGATAGTTTTGCACTTTACACAACGTGAACAAGACAAATTGATGAT
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OTHER INFORMATION: Description of Artificial Sequence: synthetic;

OTHER INFORMATION: nucleic acid sequence

US-10-793-626-4032
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                                                                                                                                                                                                                                                   Length 3475;
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                                                                                                                                                                                                                                                 DB 1;
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Pred. No. 1.6e-93;
1; Mismatches 762;
                                                                                                                                                        TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.1%;
Matches 1010; Conservative
 GENERAL INFORMATION:
                                                                                                                              SEQ ID NO 4032
                                                                                                                                             LENGTH: 3475
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NS-10-193-626-115

Sequence 115, Application US/10793626

Publication No. US2005025547841

Publication No. US2005025547841

TITLE OF INVERMITON: TAPHTLACCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

TITLE OF INVERMITON: TAPHTLACCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

CURRENT APPLICATION NUMBER: US/10/793,626

CURRENT FILING DATE: 2004-03-04

PRIOR APPLICATION NUMBER: 60/164,258

NUMBER OF SEQ ID NOS: 4472

SOFTWARE: PALENTIN Ver. 2.1

SEQ ID NO 115

LENGTH: 336
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic; ; OTHER INFORMATION: nucleic acid sequence US-10-793-626-121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
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                                                                                                           Length 309
                                                                                                           Score 97.4; DB 1; Length 3 Pred. No. 7.9e-15; 0; Mismatches 121; Indels
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                                                                                                                3.4%;
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                                                                                                           Query Match
Best Local Similarity 59.4'
Matches 186; Conservative
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                                                                   Sequence 2, Application US/10834151
Publication No. US20050244836A1
Publication No. US20050244836A1
GENERAL INFORMATION:
APPLICANT: TSANG, TAT-KIN
APPLICANT: ZHANG, HONGJUN
TITLE OF INVENTION: METHODS AND COMPOSITIONS TO DETECT BACTERIA USING MULTIPLEX PCR
FILE REFRERENCE: 37611-95516
CURRENT APPLICATION NUMBER: US/10/834,151
CURRENT FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 20
SEQ ID NO 2
LENGTH: 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1080 GAAAACACCCTAGATTTAGTCATTAACGCGATGATTATCGACTACACCGGGATTTAC 1139
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Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SEQ ID NO 121
LENGTH: 309
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Pred. No. 1.7e-43;
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, ORGANISM: Helicobacter pylori
US-10-834-151-2
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Sequence 4389, Application US/10793626

Publication No. US20050255478A1

GENERAL INFORMATION:
APPLICATION:
APPLICATION
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60164.258
PRIOR APPLICATION NUMBER: 60164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4389
LENGTH: 3373
774 TIGGIGGCAGIAAAAAAGIGAIIGGCAIGAACGGGCIIGIGAAIAACAICGCGGAIGAA 832
                                              185 ATTCTGGACGAAAATTTATGGATTCCGTGGTTTAGTCGATGGCGATATTGACGAA 243
                                                                                                                                                                                                                                                APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STARHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILL REFERENCE: PU3480US
CURRENT EPILICATION NUMBER: US/10/793,626
PURRENT FILLING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILLING DATE: 1999-11-09
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                                                                                                                                                                        Sequence 4078, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
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Matches 158; Conservative
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SOFTWARE: Patentin Ver. 2.1
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LENGTH: 2259
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TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPRESENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PILING DATE: 1999-11-09
NUMBER OF FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4109
LENGTH: 3923
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-4389
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                                                                                                                                                                        DB 1; Length 3373;
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                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                           48;
                                                                                                                                                                           1.4%; Score 40; DB 1
56.8%; Pred. No. 2.1;
tive 3; Mismatches
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56.8%; Pred. No. 2.3;
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; Publication No. US20050255478A1
; GENERAL INFORMATION:
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LENGTH: 3927
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                        Query Match
Best Local Similarity 56.8'
Matches 67; Conservative
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Matches 67; Conservative
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US-10-793-626-4109/c
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SEQ ID NO 4132
LENGTH: 2988
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                                                                                                                                                                                                53 AAATTRCRACTTGTTAATRCTATTATTAATTTTTTAATAATTACTTATTATCATATAA 112
                                                                                                                                                                                                                                                                             113 TAATATTATTACTTATATAAAAAGTTAATAAAAAGTAACGAAATTAGGACTATAATCCC 172
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Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KINMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KINMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
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                    FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic OTHER INFORMATION: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-2361
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                                                                                                                   Length 3923
                                                                                                                                                          58; Indels
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                                                                                                                   Score 39.8; DB Pred. No. 2.6;
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Publication No. US20050255478A1
GENERAL INFORMATION:
                                                                                                                   1.4%;
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                               1983 ACAAGTATTATAA 1971
                                                                                                                                                                                                                                                                                                                                                          173 ATTGCCTTTAAAA 185
                                                                                                                                   Best Local Similarity 55.6
Matches 74; Conservative
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                                                                             US-10-793-626-4109
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LENGTH: 1809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 CTTATATAAAAAGTTAATAAAAAGTAACGAAATTAGGACTATAATCCCATTGCCTTTAA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4132, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: KIMMERLY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPERENCE: PUJ48003
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PLING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                    23 AGCACATATTGATCCTGTGTTGTGGGTGGTAAATTRCRACTTGTTAATRCTATTATTAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic; ; OTHER INFORMATION: nucleic acid sequence
US-10-793-626-4132
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                                                                                                                                                                                                                                                                                                                1.3%; Score 37.8; DE 53.3%; Pred. No. 7.5; tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.3%; Score 37.2; Di
illarity 52.7%; Pred. No. 9.5;
Conservative 1; Mirr-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 TACTTGTCATAATGACAAATATATATA 362
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PRIOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4033
LENGTH: 3591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2864 GAGAACGTCCACAT 2850
                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 AAAAAGTAACGAAAT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.33
Matches 72; Conservative
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Best Local Similarity
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us-09-904-994b-1.rni

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Sequence 1, Appli
Sequence 22, Appl
Sequence 22, Appl
Sequence 1857, App
Sequence 258, App
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 241, Appl
Sequence 241, Appl
Sequence 2045, Appl
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Sequence 1, Appli
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Sequence 1, Appli
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9817.453 Million cell updates/sec
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Sequence 1, Aps
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-432-697-19

US-08-446-248-19

US-09-431-705-1

US-09-431-705-1

US-09-431-705-1

US-09-613-105-1

US-08-667-645B-1

US-08-667-645B-1

US-08-67-645B-1

US-08-67-645B-1

US-09-557-884-1

US-09-557-884-1

US-09-557-884-1

US-09-557-884-1

US-09-557-884-1

US-09-557-884-1

US-09-557-884-1

US-09-453-004-1

US-09-453-004-1

US-09-453-702B-57

US-09-453-702B-57

US-09-453-702B-57

US-09-487-429A-3

US-09-487-429A-3

US-09-487-429A-3

US-09-489-033A-2045

US-09-10-114-170-57

US-09-489-033A-2045
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Maximum Match 100%
Listing first 45 summaries
                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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36.7 4824
25.6 6131
24.1 2400
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Sequence 3853, Ap
Sequence 117, App
Sequence 1289, Ap
Sequence 1786, Ap
Sequence 10346, A
Sequence 10546, A
Sequence 13, Appl
Sequence 13, Appl
Sequence 2, Appl
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Sequence 4032, Ap
Sequence 10513, A
Sequence 10653, A
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Sequence 159, App
Sequence 7520, Ap
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Sequence 1913,
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APPLICATUR: Cynthia K. Lee et al.

TITLE OF INVENTION:

MULTIMERIC, RECOMBINANT UREASE VACCINE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
COMPUTER: READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,095
FILING DATE: 28-APPL-1995
ATTORNEY/AGENT INFORMATION:
PRIOR APPLICATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/013001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFPHONE: (617) 542-5070
US-09-710-279-3853
US-09-710-279-117
US-09-714-001C-2189
US-09-328-352-1786
US-09-252-991A-10316
US-09-62-777A-13
US-09-602-777A-13
US-09-602-777A-13
US-09-601-198-89
US-09-601-198-89
US-09-103-840A-1
US-09-103-840A-1
US-09-103-840A-1
US-09-252-991A-10653
US-09-252-991A-10653
US-09-252-991A-10653
US-09-253-991A-10653
US-09-253-991A-10653
US-09-543-681A-1913
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08920095; Patent No. 5837240; GENERAL INFORMATION:
                                               1722
1704
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1625
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441155
3475
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TYPE: nucleic acid
STRANDEDNESS: double
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502
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213.2
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Gaps

Score 1075.2; DB 2; Length 2735; Pred. No. 5.8e-267; 0; Mismatches 798; Indels 38;

37.3%; ilarity 66.0%; Conservative 0

Query Match Best Local Similarity Matches 1622; Conserv

1155 CITAGOTRAGICCOCCATICOTTCCCACACAAATTCCCTACACCACCACCACCACCACCAC
6 H 6 H 6 H 6 H 6 H 6 H 6 H 6 H 6 H 6 H
122 ANAITTIANCHCARGAGTAATAAGTGAAACTCACCAAAGAAAACTCATTAATTA

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                                                                                     CAAGTICTACCGGTCAAAAACTGCCGTAACATCACCAAGAAAGACTTCAAGTTCAACGAC 2486
                                                                                                                 CAAGTGTTGCCGGTAAAAATTGCAGAAATATCACTAAAAAAGACATGCAATTCAACGAC 2414
                                                                                                                                               AAAACGGCAAAAATCACCGTCGAAAAACCTTCGAGGTCTTTGTAGATGGCAAACTC 2546
                                                                                                                                                                          2415 ACTACTGCTCACATTGAAGTCAATCCTGAAACTTACCATGTGTTCGTGGATGGCAAAGAA 2474
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CCGGTTTATTACAGAGAAATGTTCGCTCATCATGGTAAAGCTAAATACGATGCAAACATC 2294
                                                         ACTTTTGTGTCTCAAGCGGCTTATGACAAAGGCATTAAAGAAGAATTAGGACTTGAAAGA 2354
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                                                                                                                                                                                                                                   2475 GTAACTTCTAAACCAGCCAATAAAGTGAGCTTGGCGCAACTCTTTAGCATTTTCTAGG 2532
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                                                                                                                                                                                                                                                                                                                                       APPLICANT: OraVax, Inc.
TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.3%; Score 1075.2; DB 6; Length 66.0%; Pred. No. 5.8e-267; cive 0; Mismatches 798; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENY APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05800 FILING DATE: 23-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
NATORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFREENCE/POCKET NUMBER: 06132/020001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                              E: Fish & Richardson P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9605800 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08/568,122
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APPLICATION NUMBER: 08/56
FILING DATE: 06-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 28-APR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2735 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 66.0
Matches 1622, Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
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                                                                                                                                                                    GTAGAAGCAGTAGCTTTGATTAGTGCCCATATTATGGAAGAAGAGCGAGAGCTGGTAAAAAG 257
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                                                138 crccacracecregagaarregeraaaaacecaaagaaaagecarraaecrraacra 197
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                                                                                                             CCCGAAGCCATTGCTTACATTAGTGCCCATATTATGGACGAAGCGCGCCGTGGAAAAAA
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                                                                                                                                                                                                                                                                                                                                                    GGGGTGGGTAATATGGTTCCCGATCTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAA
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USE IN THE ENCODING SAID
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                                                                                                           2427 CAAGTICTACCGGICAAAAACIGCCGIAACAICACCAAGAAAGACTICAAGIICAAGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Friberge, Jean-Michael L.
APPLICANT: Thiberge, Jean-Michael L.
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES TITLE OF INVENTION: POLYPEPTIDES NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature
LOCATION: 31..36
OTHER INFORMATION: /standard_name= "Shine-Dalgarno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MM-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET UNBER: 03495.0137-02000
TELECOMMUNICATION:
TELECOMMUNICATION: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Finnegan, Henderson, Farabow,
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
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FILING DATE: 06-JUN-1995
CLASSIPRICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 19, Application US/08467822
Patent No. 5843460
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 2619 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Labigne, Agnes
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STRANDEDNESS: double
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                                                                                                                                                                                                                               GAAGCGGGCGCGATTGGTTTTAAATTGCATGAAGACTGGGGCACAACACCAAGTGCGATC 1586
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  GGAATCGATTCACACCCCACTTCCTTTCTCCACAACAATTCCCTACCGCTCTAGCCAAT 1346
                                                                                                                                                                                                                                                                                                                                             AATTTAGGTTTCTTGGCTAAAGGTAACGCTTCTAACGATGCGAGCTTAGCCGATCAAATT 1454
                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGCCGGTGCGATTGGCTTTAAAATTCACGAAGACTGGGGCACCACTCCTTCTGCAATC 1514
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                                   GAGCTCAATATTCTACCCTCCTCCACCACCCCCCTATTCCCTATACCGTT
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                                                                                                                                     GGCGGTATGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCCACTCCCCAA
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                                                              Score 1062.6; DB 2; Length
Pred. No. 1e-263;
0; Mismatches 804; Indels
36.9%;
ilarity 65.5%;
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                                                                         NAME/KEY: misc feature
LOCATION: 31..36
O'THER INFORMATION: /standard name= "Shine-Dalgarno
O'THER INFORMATION: sequence."
FEATURE:
NAME/KEY: misc_feature
LOCATION: 756..759
O'THER INFORMATION: /standard_name= "Shine-Dalgarno
O'THER INFORMATION: sequence."
US-08-432-697-19
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Pred. No. 1e-263;
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GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: OOMPOSITIONS, AND NUCLRIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
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GGATCGCGCATGGGATTTCTGACTATGTGGGCTCTGTGGAAGTGGGCAAATACGCCGACC 2065
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/08432697
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1300 I Street, N.W.
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 19:
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US-08-432-697-19
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US-08-46-218-19

US-08-48-19

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              GGATCGCGCATGGGATTTCTGACTATGTGGGCTCTGTGGAAGTGGGCAAATACGCCGACC
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COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 19-MAX-1995
CLASSIFICATION: 435
FRIOR APPLICATION: 435
CLASSIFICATION: 435
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Pred. No. 1e-263;
0; Mismatches 804; Indels
                                                                                                                                                                                                                                                                                                            NAME/KEY: misc_feature
LOCATION: 31..36
OTHER INFORMATION: /standard_name= "Shine-Dalgarno
OTHER INFORMATION: sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
COCATION: 756..75
COCHER INFORMATION: /standard_name= "Shine-Dalgarno
OTHER INFORMATION: sequence."
                         AREAL LOSTION NUMBER: US 08/432,697 FILING DATE: 02-MAY-1995 CLASSIET CARE
                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
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Best Local Similarity 65.5%;
Matches 1606; Conservative
PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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1946 AAGGCGATAACGACAACTTCCGCATCAAACGCTACATCTCTAAATACACCATCAACCGG 2005
                                                                                                                              GTGTGATCGCGATGACAAGCTCGGATTCGCAAGCAATGGGGCGTGCAGGCGAAGTGATTC 2013
                                                                                                                                                                                                                              CTCGAACTTGGCAGACTGCGGATAAGAATAAAAAGAATTTGGTAAGCTTCCTGAAGATG 2073
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  ACTTAGACATGCTCATGACATGCCACCCACCTAGACAAACGCATCCGCGAGGATTTACAAŢ 1893
                                                                                                  TTTCTCAAAGCCGTATCCGCCCCGGCTCTATCGCGGCTGAAGATGTGCTCCATGATATGG
                                TGGTGGTCTTCTCTGAAATGGGCGATTCTAACGCGTCTGTGCCCCACTCCCCAACCGGTTT
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APPLICANT: Londono-Arcila, Patricia
APPLICANT: Freeman, Donna
APPLICANT: Freeman, Donna
TITLE OF INVENTION: Use of Salmonella vectors for
TITLE OF INVENTION: vaccination against helicobacter infection
FILE REFERENCE: 06132/060001
CURRENT APPLICATION NUMBER: US/09/431,705
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
FEATURE:
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INFORMATION: includes sequences from Helicobacter pylori, INFORMATION: Salmonella typhimurium, and Escherichia coli
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; Patent No. 6585975
; GENERAL INPORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Freeman, Donna
; TITLE OF INVENTION: Use of salmonella vectors for
; TITLE OF INVENTION: Use of salmonella vectors for
; FILE REPRENCE: 06132/060001
; CURRENT APPLICATION NUMBER: US/09/431,705 GCCAATAAAGTGAGCTTGGCCCAACTCTTTAGCATTTTCTAGG 2562 ACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTTAGG

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 Arccardaagregerarreaagcearerrrecrearegeacraaacregraacegreer 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACATCACTATCAACGAAAGGCAAAAAGCCGTTAGCGTGAAAGTTAAAAATGTTGGCGAC 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GACATCGAGCTCAATGCAGGCAAAGAAGTAACCGAACTTGAGGTTACTAATGAAGGGCCT
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                                                                                                                                                                                                          includes sequences from Helicobacter pylori, Salmonella typhimurium, and Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 36.7%; Score 1058.6; DB 3; Best Local Similarity 65.7%; Pred. No. 1.4e-262; Matches 1606; Conservative 0; Mismatches 799;
                                 JS: 52
for Windows Version 4.0
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Ve
SEQ ID NO 19
                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                   NAME/KEY: CDS
LOCATION: (1893)...(3934)
NAME/KEY: CDS
LOCATION: (1993)...(4027)
NAME/KEY: CDS
LOCATION: (4031)...(4285)
NAME/KEY: CDS
LOCATION: (4289)...(4300)
NAME/KEY: CDS
LOCATION: (4289)...(4408)
NAME/KEY: CDS
LOCATION: (4412)...(4471)
NAME/KEY: CDS
LOCATION: (4412)...(4471)
NAME/KEY: CDS
LOCATION: (4412)...(4588)
NAME/KEY: CDS
LOCATION: (4475)...(4588)
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LOCATION: (4784)...(4824)
US-09-431-705-19
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ZIP: 10016-2088

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72mb

COMPUTER: 18M PC compatible (NEC PC-9801 RX)
COMPUTER: 18M PC compatible (NEC PC-9801 RX)
COFTWARE: ASCII Form

CURENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732,242C
FILING DATE: 19910718
CTASSIFFCATION: 435
PRIOR APPLICATION NUMBER: JPN 2-210178
APPLICATION NUMBER: JPN 2-210178
APPLICATION NUMBER: JPN 2-210178
ATTORNEY AGENT INFORMATION:
ATTORNEY AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Goodman, Herbert
REGISTRATION NUMBER: 17081
REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 6131 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212)370-1622
TELEX: 236268
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 1442; Conserv
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Patent No. 5298399

GENERAL INFORMATION:
APPLICANT: Uozumi, Takeshi; Masaki, Haruhiko;
APPLICANT: Hidaka, Makoto; Nakamura, Akira;
APPLICANT: Madda, Michihisa; Yoneta, Yasuo
TITLE OF INVENTION: Gene of Urease
NUMBER OF SEQUENCES: 14
CORRESSONDENCE ADDRESS:
ADDRESSEDS: Frishauf, Holtz, Goodman & Woodward, P.C.
STREET: 600 Third Avenue
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                                             ---AGATAGCCCTGAATACCGGCCGGCAACCTGTCGCGTGGTCGTTGAGAACCACGGCG
                                                                                                                                434 ATCGGCCGATTCAGGTCGGTTCGCACTACCATTTCGCCGAGGTTAACCCCGGCGCTGAAGT
                                                                                                                                                                            TCGATCGTGAAAAAGCCTATGGCAAACGCCTAGATATTCCCTCTGGCAACACGCTACGCA
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        555 AAGACATCGAGCTCAATGCAGGCAAAGAAGTAACCGAACTTGAGGTTACTAATGAAGGGC
                                                                                       CTAAATCCTTGCATGTGGGTAGCCATTTCCACTTCTTTGAAGCTAACAAGGCACTAAAAT
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                          inch, 360
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 36
MEDIUM TYPE: Storage
COMPUTER: STORAGE
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION NUMBER: US/08/967,513
FILING DATE: 11-NOV-1997
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                                                                                                                                                                                     CLASSIFCATION: 435
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/687,645
FILING DATE: July 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Ian.C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.1-
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELEFAX: (517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella aerogenes
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| LOCATION: glutamine
| IDENTIFICATION METHOD:
| OTHER INFORMATION:
| US-08-967-513-1
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STRANDEDNESS: Single
TOPOLOGY: Linear
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INDIVIDUAL ISOLATE:
CELL TYPE: N/A
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DESCRIPTION:
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ORIGINAL SOURCE
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NAME/KEY:
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Mutant Urease and Method of Use For Determination of Urea: 5

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wondperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,645B
FILING DATE: July 26, 1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.
TELECOMMUNICATION INFORMATION:
TELEFRONE: (517) 347-4103
             APPLICANT: Robert P. Hausinger
TITLE OF INVENTION: Mutant Urease
TITLE OF INVENTION: of Use For De
TITLE OF INVENTION: of Use
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                  ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: No. 5846752e
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: Sin
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DESCRIPTION: CDNA
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                                                                                                                                                                                                                 Michigan
GENERAL INFORMATION:
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CITY: Okemos
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ANTI-SENSE: N
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                                                                                                                                                                                                     ACCGCCTGCGCCCACCCGAACATTTTGCCGTCGTCCACCAACCCAACGCTGCCCTACACC 1570
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                                                                                     CGCGCCATCCATGCCTACCACATTGAGGGAGCGGGTGGAGGACACTCACCTGATGTTATC 1754
                                                                                                                                                                      ACCATGGCAGGCGAGCTCAATATTCTACCCTCCACCACCCCCCACTATTCCCTATACC 1814
                                                                                                                                                                                                                                                           ATTAATACGGTTGCAGAACACTTAGACATGCTCATGACATGCCACCACCGTAGACAACGC 1874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2295 CCCACTCCCCAACCGGTTATTACCGCGAAATGTTTGGGCATCACGGCAAGGCGAAATTT 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2111 CACTGCCGCCTCACCTTCCTGTCGCAGGCGGCAGCCAATGGCGTTGCCGAGCGGCTG 2170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2475 AAGTICAACGACAAAAACGGCAAAAAICACCGICGAICCGAAAACCITCGAGGICTTIGIA 2534
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CACACCGATACAGTCAATGAGGCAGGTTATGTAGATGACACCCTAAATGCAATGAACGGG 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2175 GAGGGCAAGATCGCCGACTTGGTGGTGTGGAATCCTGCCTTTTTTGGCGTAAAACCCAAA 2234
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                          1391 CACAGGGACACCCTGAATGAATCCGGTTTTGTGGAAGACACCCTCGCCGCCGTCGGGGG
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Sequence 1, Application US/08687645B Patent No. 5846752

RESULT 10 US-08-687-645B-1

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564897 ATAATAAATTAAGGAATGAAATATGCACTTAACTTCCAGAGAACAAGAAAAACTGATGC
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                                                                                                                                                    RESULT 11
US-09-557-884-1/C
; Sequence 1, Application US/09557884
; Patent No. 650581
; GENERAL INFORMATION:
; APPLICANT: Pleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of
; TITLE OF INVENTION: The Haemophilus influenzae F
                                                                                                                                                                                                                                                                                                                                              STREET: 9410 Key West Avenue CITY: Rockville STATE: MD COUNTRY: USA ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.0%; Score 664.4; DB 3;
llarity 57.1%; Pred. No. 1.1e-159;
Conservative 1; Mismatches 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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APPLICATION NUMBER: 08/476,102
                                                          TTCTTCTAGGCACAATGCCCCCTTT 2619
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                                                                                                    2351 CTGTTTTAAGGAGAGGGGATGCTTT
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human G
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Best Local Simil
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564897 ATAATAAATTAAGGAATGAAAATATGCACTTAACTTCCAGAGAAGAAGAAAACTGATGC 564838
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                                                                                                                                                                                                                                                                                                               Hamilton O. Smith
J. Craig Venter
J. Craig Venter
INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
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  562507 AACCAGTGGATAGCGTACCATTGGGTCAGCGATATTTCCTATTCTA 562462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 664.4; DB 3;
Pred. No. 1.1e-159;
1; Mismatches 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville, STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PB186P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/487,429
                                                                                                                                                                                                                        APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
                                                                                RESULT 12
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 301-610-5790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 310-309-8439
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STRANDEDNESS: double
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Matches 1397; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20850
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-643-990A-1
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	Oy         1477 TTTTGGGCAAAGGCAATAGCTCTAGCAAAAAAACAC           Db         563581 TTTTTGTTAAAGGCAACTGTTCACCTAGATCTC           Oy         1537 CGATTGGTTTAAATTGCATGAAGACTGGGGCACAA           Oy         1637 CATTAGGTTTTAAATTGCATGAAGACTGGGGGCACAA           Db         563521 CATTAGGTTTAAAAAACCACAAGAGACTGGGGTCCAA	1597	Oy 1657 CAGGTTATGTAGATGACCCCTAAATGCAATGAACG	OY 1717 TTGAGGGAGGGGTGGAGGACACTCACTGATGTTA'	1777	1837 563221	1897 563161	Qy 1957 TGATCGCGATGACAAGCTCGGATTCGCAAGCAATGG 	2017	Oy 2017 AAGATAACGATAATTTCCGCATTAAGCGCTACATCTV	OY 2137 TGACCCACGGCGTGAGGGAGTATATCGGCTCTGTGG DD 562927 TTGCACATGGTATTGCGGAGCATATTGGCTCGTTAG	2197 562867	2257 562807	Oy 2317 ACCGCGAAATGTTTGGGCATCACGGCAAGGGGAAAT 	Qy 2377 CCAAAGTCGCCTATGAAAATGGCGTGAAAGAAAAGC' Db 562687 CACAAGCCGCTGAAAAAGCTGATATTCGTGCGAAGT	OY 2437 CGGTCAAAACTGCCGTAACATCACCAAGAAAGACT" Db 562627 CTGTGAAAGGCTGCCGCAACGTAGGTAAAAAGATC"	2497 AAATCACCGTCGATCCGAAAACCTTCGAGGTCTTTG	2557
-	423 GGGTGGGTAATATGGTTCCCGATCTAGGTGTAGAGCCACCTTTCCTGATGGTACGAAAC 482	564600 TTGTTACCGTGCATACATAACCGWAGGGTGGGCTTTAGCCCACAAATAAA 564541 539 AAATTTGGTTGCGATAAAGACATCGAGCTCAATGCGGCAAAGAAGAAACGAACTTGAG 598 54540 AATATCAATGGTGGGCTCAAAGAACAAGAAAAAAATATGTCCCGAAT 564481	599 GTTACTAATGAAGGGCCTAAATCCTTGCATGTGGGTAGCCATTTCCACTTTTGAAG 656	SOUTH OF ACCEPTANCE AND ACCEPTANCE	564360 ATANCARATICAGGCARCCGCATTGGGGCAGGACGCGCAAAGTGCATTTTTTTTTGAACCA 564361 711 TTCCCTCTGGCAACACGCATTGGGGCAGGACACCCGCAAAGTGCAGTTGATTC 770	771 CTCTTGGTGGCAGTAAAAAGTGATTGGCATGAACGGGCTTGTGAATAACATCGCGGATG 830		889 AGACTCCCATGAAAATGAAAAACAAGAATATGTAAATACCTACGGACCCACCAAAGGCG 948	949 ATAMAGTGCCTTAGGGGTACCCATCTTGGGCAAAACAAACATATACCACCT 1008	1009 ATGGCGAAGAACTTAAATTTGGCGCGGGTAAAACTATCCGTGAGGGTATGGGTCAGAGC- 1067	1068AATAGCCCTGATGAAACACCCTAGATTTAGTCATCACTAACGCGATGATTA 1119    AATAGCCCTGATGAAACACCCTAGATTTAGTCATCACTAACGCGATGATTA 1119	1120 TCGACTACACCGGGATTTACAAGCCGACATTGGGATTAAAACGGCAAAATCCATG 1176  1130 TCGACTACACCGGGATTTACAAGCCGACATTGGGATTAAAACGGCAAAATTGGGATTACAAAGCCGATATTCGTGATGGGCGTATTGTGG 563882	1177 GCATTGGCAAGGAACAAGGACATGCAAGATGGGTAAGCCCTCATATGGTCGTGG 1236	1237 GTGTGGGCACAGAAGCACTAGCAGGGAAGGTATGATTATTACCGCTGGGGGAATCGATT 1296 553831 GTGTAGGCACAGAAGGTAAGGAAAGGTATGATTATTACCGCTGGGGGAATCGATT 1296 553831 GTGTAGGAAGGTAAGAAGAAGAAGAAGAAGAAAGAAGAAG	1297 CACACACCACTTCCTCCCAAACAATTCCCTACCGCTCTAGCCATGCGTTACAA 1356	563761 CCCACATTCACTTTATTTGTCCACAACAACATGCAATTGAAAGTGGCGTTACCA 563702 1357 CCATGTTTGGAGGCGCCACAGGTCCTGAAGGCGCACAATGCGACTACCACTCCGG 1416	563701	563641 GCGCATGGTATATGGAACGTATGTTTCAAGCGGCAGAAGCCTTGCCGGTAAACGTCGGAT 563582
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CTTGTAGAACAAGTAGAAGCGGGCG 1536 CAAGATGTGCTCCATGATATGGGTG 1956 TCCAAATACACTATCAACCCGGTT 2136 GTGCCCACTCCCCAACCGGTTTATT 2316 ATTAAAGCAGCGATGTATTCAAACG 563282 CCCCCCCCCCAACCTTTTG 563162 REGEGGGGGGGGAAGTGATICCTC 2016 |||| |||| |||| |CGTGGTGAGCTAGGTAATGAAGGA- 562983 GAAGAGGGCAAGATCGCCGACTTGG 2196 GCACAAACAGCAGTATTCTTTGTTT 562688 rrcgerrracacaagaaccarrg 562628 CIGGTTCATATGATGTAACACCAA 562568 Gredacedasacriaartaccrere 562508 TTTGGTAAGCTTCCTGAAGATGGCA 2076 ACACCAAGTGCGATCGATCACTGCT 1596 ATCCACACCGATACAGTCAATGAGG 1656 GGGCGCCCATCCATGCCTACCACA 1716 ATCACCATGGCAGGCGAGCTCAATA 1776 ACCATTAATACGGTTGCAGAACACT 1836 CGCATCCGCGAGGATTTACAATTTT 1896 AAAATCGTGATCAAAGGCGGTATGG 2256 TTTGACACCAGCATCACTTTTGTTT 2376 CIGGGCTTAGAGCGCCAAGTTCTAC 2436 GTAGATGGCAAACTCTGCACCTCTA 2556 TTCAAGTTCAACGACAAAACGGCAA ACTITCTICIA 2602

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LOCATION: (119924)..(119924)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (107248)..(107248)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (51602)..(51602)
OTHER INFORMATION: n equals a,t,c, or
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NAME/KEX: misc_feature
NACATION: (51805)..(51805)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (55369)..(55369)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (51786)..(51786)
OTHER INFORMATION: n equals a,t,c, or
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                     LOCATION: (45593) .. (45593)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (47036)..(47036)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (51334)..(51334)
OTHER INFORMATION: n equals a,t,c, or
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LOCATION: (80024)..(80024)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (65309)..(65309)
JTHER INFORMATION: n equals a,t,c,
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LOCATION: (65313)..(65313)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (100091)..(100091)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (105<u>1</u>21)..(105121)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (119750)..(119750)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (45732)..(45732)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (102696)..(102696)
OTHER INFORMATION: n equals
    NAME/KEY: misc feature
LOCATION: (45593)..(459
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NAME/KEY: misc_feature
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                                                                                                        US-2011-158-865-1/C

Sequence 1, Application US/10158865

Patent No. 6846651

APPLICANT: Fleischmann et al.

TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus Influenzae Rd Genome, Fragging Price Programmer Price of the Haemophilus Influenzae Rd Genome, Fragging Price of INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION: Thereof, and Uses Thereof

FILE REPRESENCE: PB186P2C1D1

CURRENT APPLICATION NUMBER: US 09/557,884

PRIOR APPLICATION NUMBER: US 09/557,884

PRIOR PLING DATE: 2000-04-25

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-04-21

NUMBER OF SEQ ID NOS: 1

SOFTWARE: Patentin version 3.1
562507 AACCAGTGGATAGCGTACCATTGGGTATTTCCTATTCTA 562462
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LOCATION: (44975)..(44975)
OTHER INFORMATION: n equals a,t,c, or g
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NAME/KEY: misc feature
LOCATION: (9921). (9921)
OTHER INFORMATION: n equals a,t,c, or
FEATURE:
NAME/KEY: misc feature
LOCATION: (10150)
OTHER INFORMATION: n equals a,t,c, or
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ORGANISM: Haemophilus influenzae
FEATURE:
NAME/KEY: misc feature
LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (36543)..(36543)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (44416)
OCHER INFORMATION: n equals a,t,c,
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LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (36636)..(36636)
OTHER INFORMATION: n equals a,t,c,
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NAME/KEY: misc_feature
LOCATION: (40808)..(40810)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (44905)..(44905)
OTHER INFORMATION: n equals a,t,c,
FEATURE:
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals a,t,c,
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                                   564777 cagajactratricctratriccractratriacaacacacac---aacacaaccaatca 564721
                                                                                                                                                                                          564660 greregegaareerreargagecegarreaageeracriceereergegegegegegege
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                                                                                                                 564720 gráradcegagreardcaracaarategegaacacririraacegreárdardreargaad
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CCGAAGCCATTGCTTACATTAGTGCCCATATTATGGACGAAGCGCCCCGTGGAAAAAAA
                                                                                                                                                        GGGTGGGTAATATGGTTCCCGATCTAGGTGTAGAAGCCACCTTTCCTGATGGTACGAAAC
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                                                                           599 GTTACTAATGAAGGCCTAAATCCTTGC--ATGTGGGTAGCCATTTCCACTTCTTTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCTTGGTGGCAGTAAAAAGTGATTGGCATGAACGGGCTTGTGAATAACATCGCGGATG
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Pred. No. 1.1e-159;
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                                                         NAME/KEY: misc feature
LOCATION: (121344)..(121344)
OTHER INFORMATION: n equals a,t,c,
                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (131340)..(131340)
OTHER INFORMATION: n equals a,t,c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (142750)..(142750)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (147<u>1</u>97)...(147197)
OTHER INFORMATION: n equals a,t,c,
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LOCATION: (150841)..(150841)
OTHER INFORMATION: n equals a,t,c,
                     INFORMATION: n equals a,t,c,
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LOCATION: (145942)..(145942)
OTHER INFORMATION: n equals a,t,c,
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Best Local Similarity 57.1%;
Matches 1397; Conservative
                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (122167)..(122167)
OTHER INFORMATION: n equals
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LOCATION: (122336)..(122336)
OTHER INFORMATION: n equals
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LOCATION: (140398)..(140398)
OTHER INFORMATION: n equals
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LOCATION: (145058)..(145058)
OTHER INFORMATION: n equals
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NAME/KEY: misc_feature
LOCATION: (145171) .. (145171)
OTHER INFORMATION: n equals
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LOCATION: (131360)..(131360)
OTHER INFORMATION: n equals
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LOCATION: (139910)..(139910)
OTHER INFORMATION: n equals
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals
   (120038)..(120038)
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562627 CTGTGAAAGGCTGCCGCAACGTAGGTAAAAAGATCTGGTTCATAATGATGTAAACACCAA 562568
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Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tractrostratoraearantagearrantarantarrangeranteranteranda 4029
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                                                            2497 AAATCACCGTCGATCCGAAAACCTTCGAGGTCTTTGTAGATGGCAAACTCTGCACCTCTA
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                                                                                                                                                                                                                                           562507 AACCAGTGGATAGCGTACCATTGGGTCAGCGATATTTCCTATTCTA 562462
                                                                                                                                                                                     AACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTTCTA 2602
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ZIP: 20850
COMPUTER: DESCRIPTION OF THE COMPUTER: DISKELTE, 3.50 inch, 1.4MD storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS Version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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55.5%; Pred. No. 2.1e-160;
iive 1; Mismatches 1093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <UNKNOWN>
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SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-08-956-171E-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
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ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                                                                                       RESULT 14
US-08-956-171E-22/c
; Sequence 22, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patrick S. Dillon
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STRANDEDNESS: double
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Gil H. Choi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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Best Local Similarity 55.5
Matches 1437; Conservative
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TCTTCTCCATTATGAGTTCAGACTCTCAAGCGATGGGACGTATTGGCGAAGTCGTTATTC 563042
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US-08-781-986A-22/c
US-08-781-986A-22/c
; Sequence 22, Application US/08781986A
; Fatent No. 673748
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; CORRESPONDENCE ADDRESS:
; CORRESPONDENCE ADDRESS:
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                                                                                                                            TAACAGTGCAACACCTAAATTAGACGTTGATCCACAAACATATGAAGTATATGTAGATGG
                                                                                                                                                                                                                                                                                                CAAACTCTGCACCTCTAAACCCACCTCGCAAGTGCCTCTAGCCCAGCGCTACACTTTCTT
                                                                                                                                                                                                                                                                                                                                        AGAAAAAATTACAAGTAATGCAGCAACTGAGTTACCATTAACTCAAAGATACTTCTTATT
                                                                                                                                                                                                               CAACGACAAAACGGCAAAAATCACCGTCGATCCGAAAACCTTCGAGGTCTTTGTAGATGG
                                         CAGCATCACTITIGITICCAAAGTCGCCTATGAAAATGGCGTGAAAAAAAAGCTGGGCTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.0%; Score 662.8; DB 3; Length 5966;
55.5%; Pred. No. 2.1e-160;
iive 1; Mismatches 1093; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/781,986A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Benson, Bob
REGISTRATION NUMBER: 30
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5966 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 5966 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 1437; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 CTAGGCACAA 2609
                                                                                                                                                                                                                                                                                                                                                                                                                         CTAGGAGGAA 1568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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295 289 289 277 277 271 151 151 151 163 259 259	CGATACAGTCAATGAGGCAGGTTATGTAGATGACCCTAAATGCAATGAACGGCGCGC 1699	193 223 199 217 205 211 205	CACTATCAACCCCGCTTTGACCCCAGGCGTGAGCGGCTATCGGCTCTGTGGAAGAGGG 2179  TACAATTAACCCAGCAATTACACATGGTATTTCTGAATATGATCTTTCGAGCCGG 1998  CAAGATCGCCGACTTGGTGGTGTGGAATCCTGCCTTTTTTTGGCGTAAAACCCAAATCGT 2239
	1640 CGA 2537 AGA 1700 CAT 2477 ACT 1760 GGC 1760 GGC 2417 CGC 1820 TAC		2120 CAC 2057 TAC 2180 CAA 1997 CAA 2240 GAT

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2480 CAACGACAAAAACGGCAAAAATCACCGTCGAAAACCTTCGAGGTCTTTGTAGATGG 2539
1697 TAACAGTGCAACACTAAATTAGACGTTGATCCACAAAACATATGAAGTATATGTAGATGG 1638
1937 IGTAAAGGGCGGATTAATTAACTCTGCCGTAAATGGCGATGCAAATGGTTCTATACCTAC 1878
                            2300 TCCCCAACCGGTTTATTACCGCGAAATGTTTGGGCATCACGGCAAGGCGAAATTTGACAC 2359
                                             1757 AAAACGCATGGTGCGTCCAGTTAAAATATTAGACAATTATCTAAAGCAGATATGAAAA 1698
                                                                                                                                                                                                                                                 2540 CAAACTCTGCACCTCTAAACCCACCTCGCAAGTGCCTCTAGGCCCAGGGGTACACTTTCTT 2599
                                                                                                                                                                                                                                                                           1637 AGAAAAATTACAAGTAATGCAGCAACTGAGTTACCATTAACTCAAAGATACTTCTTATT 1578
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Search completed: November 29, 2005, 07:30:10 Job time : 550 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

November 28, 2005, 08:00:02 ; Search time 14.5164 Seconds (without alignments) 1497.963 Million cell updates/sec

1181 1 VKLTPKBQEKFLLYYAGEVA......ADERHKHKALDKAKSHGFIK 226 US-09-904-994B-2 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

pirl:\* pir2:\* pir3:\* PIR\_80:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	urease alpha chain	(EC 3.	ო	urease, beta/gamma	urease (EC 3.5.1.5	probable urease F1	(EC 3.	m.	urease (EC 3.5.1.5	probable ureA prot	urea	В	٠:	urease (gamma subu	3.5	urease (EC 3.5.1.5	۳. ت	m.	E E	Ξ.	e c	urease (EC 3.5.1.5		urease gamma chain		urease (EC 3.5.1.5	urease gamma subun	urease gamma subun	urease gamma chain
SUMMARIES	ID	B71977	URKCAP	S35290	D75586	URJB	A96699	T37939	T29055	A36138	H70664	D85603	B90794	S74889	B69729	A36950	S47102	A64076	S38484	C90027	B47090	C69729	S08478	B43719	AD2264	E83037	S42602	D83681	AE2872	F97648
	DB	2	н	-	7	<del>, -4</del>	7	7	7	Н	7	7	~	7	7	7	~	7	-	7	7	N	Н	Н	7	~	~	7	~	0
	Length	238	238	237	228	840	838	835	227	100	100	100	100	100	105	100	100	100	137	100	100	124	100	100	100	100	100	100	100	107
æ	ራሳ	51.9	51.7	48.0	40.9	37.2	S	33.7	m.	m	23.6	m	m	m	22.9	3	~	N	~	N	2	N	N	2	~	-	21.8	_	-	21.3
	Score	613.5	610.5	566.5	483	439.5	419.5	398.5	395	281.5	278.5	277.5	277.5	276.5	271	270.5	269.5	267.5	266	265.5	264.5	263	262.5	261.5	259.5	258.5	257.5	256.5	251.5	251.5
	Result No.	-	7	٣	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	50

urease beta chain	urease (EC 3.5.1.5	urease beta subuni	urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease beta subuni	urease (EC 3.5.1.5	hypothetical prote	urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease complex com	urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease (EC 3.5.1.5	urease (EC 3.5.1.5
AE2264	S38483	D90027	A10324	S31418	\$47103	AC2872	S42604	S76224	AC3333	S31417	A82891	AB3333	T50708	I64075	AG3458
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_	00	136	100	164	126	101	101	105	100	102	101	159	100	101	101
106	Ä	-,													
	20.9	• •	20.5	20.4	20.3	20.1	20.0	19.8	19.7	19.7	19.5	19.5	19.3	19.1	19.1
20.9	•	20.7													

## ALIGNMENTS

RESULT 1

B71977	
urease	urease alpha chain - Helicobacter pylori (strain J99)
C, Speci	C.Species: Helicobacter pylori
C:Date:	#, variety: strain 0.5 C:Date: 12.Feb-1999 #sequence revision 12-Feb-1999 #text change 09-Jul-2004
C, Acces	C;Accession: B71977
R;Alm,	R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.,
; Ives,	C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature	397, 176-180, 1999
A, Title	A, Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
A;Refer	cence number: A71800; MUID:99120557; PMID:9923682
A; Acces	Ajacession: B/1977
A.Molecu	Associated by the state of the
A;Resid	As Residues: 1-238 <arn></arn>
A; Cross	A, Cross-references: UNIPROT: Q9ZMZ4; UNIPARC: UP10000137D6F; GB: AE001446; GB: AE001439; NII
A; Exper	A, Experimental source: strain J99
C;Genetics:	1.108:
A;Gene: ureA	ureA
C;Super	C;Superfamily: urease, tused gamma/Dets subunit; urease 11K chain homology; urease 12K c b:1.10/10mmsin: urease 11K chain homology (111).
F;108-2	F;108-204/Domain: urease 12K chain homology <u12></u12>
•	
Query Best	Query Matcn Best Local Similarity 53.1%; Pred. No. 1.3e-43;
Match	nes 119; Conservative 42; Mismatches 62; Indels 1; Gaps 1;
à	1 VKLTPKEQEKPLLYYAGEVARKRKAEGLKLNOPEAIAYISAHIMDEARRGKKTVAQLMEE 60
ď	:       :  :  :        :        :
}	
Ġ	61 CMHFLKKDBVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIBPDEHFKAGEVKFGCDKDIE 120
q	61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
ò	121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFRANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
î	
g	120 INEGKKAVSVKVKNVGDRFVQIGSRFRFRVNKCHDFDRENIFGGRADIASGIAVAFBFG 1.7

urease (EC 3.5.1.5) 26K chain - Helicobacter pylori (strains 26695 and others) N.Alternate names: urea amidohydrolase; urease alpha chain C.Species: Helicobacter pylori (c.Species: Helicobacter pylori (c.Species: Helicobacter pylori) Haequence revision 15-Aug-1997 #text change 09-Jul-2004 C.Accession: A38537; A64529; S07884; B35306; A41502; A61371; E49215

RESULT 2 URKCAP

181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF

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62; DB 1;

Length 238;

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1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                  51.7%; Score 610.5; DB 1
52.7%; Pred. No. 2.4e-43;
tive 43; Mismatches 62
F;1-101/Domain: urease 11K chain homology <U11>F;108-204/Domain: urease 12K chain homology <U12>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.08;
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R, Ferrero, R.L.; Labigne, A.
Mol. Microbiol. 9, 323-333, 1993
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                                                                                                                                      Best Local Similarity 52.73
Matches 118; Conservative
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Best Local Similarity
Matches 112; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                          Query Match
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A,Residues: 1-36,'R',38-48,'R',50-131,'PP',134-238 <CLA>
A;Residues: 1-36,'R',38-48,'R',50-131,'PP',134-238 <CLA>
A;Cross-references: UNIPARC:UP1000002DB17; EMBL:X17079; NID:g43633; PIDN:CAA34932.1; PID
R;Dunn, B.E.; Campbell, G.P.; Perez-Perez, G.I.; Blaser, M.J.
J. Biol. Chem. 265, 9464-9469, 1990
A,Title: Purification and characterization of urease from Helicobacter pylori.
A;Reference number: A35306; MUID:90264448; PMID:2188975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¡Bvans Jr., D.J.; Bvans, D.G.; Kirkpatrick, S.S.; Graham, D.Y.
icrob. Pathog. 10, 15-26, 1991
¡Title: Characterization of the Helicobacter pylori urease and purification of its subu ¡Reference number: A61371; WUID:91312104; PMID:1857197
                               J. Bacteriol. 173, 1920-1931, 1991
A;Title: Shuttle cloning and nucleotide sequences of Helicobacter pylori genes responsib
A;Reference number: A38537; MUID:91161505; PMID:2001995
                                                                                                                                                                                                                                                          R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.P.; Sutton, G.G.; Fleischmann, R.D. Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 388, 539-547, 1997
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the urease enzymes of Helicobacter species
PMID:1452359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-238 <TONS
A;Cross-references: UNIPARC:UPI000002C3CD; GB:AE000529; GB:AE000511; NID:g2313152; PIDN:
                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P14916; UNIPARC:UP1000002C3CD; GB:M60398; NID:g149007; PIDN R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clavton, R.A.; Sutton, G.G.; Fleischmann, R.D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: ureA; HP0073
C;Complex: heterodimer of 26K chain and 62K chain (see PIR:URKCBP)
C;Function:
A;Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and t C;Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K C;Keywords: heterodimer; hydrolase; metalloprotein
F;1-238/Product: urease 26K chain #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Nucleotide sequence of two genes from Helicobacter pylori encoding for urease A;Reference number: S07884; MUID:90221820; PMID:2326167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Infect. Immun. 58, 992-998, 1990
A;Title: Purification and N-terminal analysis of urease from Helicobacter pylori.
A;Reference number: A41502; MUID:90202165; PMID:2318539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Experimental source: strain 26695
R;Clayton, C.L.; Pallen, M.J.; Kleanthous, H.; Wren, B.W.; Tabaqchali, S.
Nucleic Acids Res. 18, 362, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPARC: UPI00000B16E0; PIDN: AAB24359.1; PID: 9260968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A, Experimental source: strain NCTC 11637
A, Note: sequence extracted from NCBI backbone (NCBIP:119486)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 1-5,'R',7-20,'R',22-30 <BVA>
A;Cross-references: UNIPARC:UPI0000172DAS
R;Turbett, G.R.; Hoj, P.B.; Horne, R.; Mee, B.J.
Infect. Immun. 60, 5259-5266, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Title: Purification and characterization A, Reference number: A49215; MUID:93084378;
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Residues: 1-13,'S',15-20 <HUA>
Cross-references: UNIPARC:UP10000172DA4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UP10000030924
R;Hu, L.T.; Mobley, H.L.T.
   R;Labigne, A.; Cussac, V.; Courcoux, P.
J. Bacteriol. 173, 1920-1931, 1991
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A;Molecule type: protein
A;Residues: 1-20 <DUN>
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                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-238 <LAB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: A41502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S07884
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A;Cross-references: UNIPROT:Q08715; UNIPARC:UPI0000137D6C; EMBL:X69080; NID:g396160; PID:
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Cloning, expression and sequencing of Helicobacter felis urease genes. A;Reference number: S35290; MUID:94018627; PMID:8412683 A;Accession: S35290
61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                         61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                  LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                           CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      120 INAGKEAISLKVKNKGDRPVQVGSHFHFFEVNKLLDFDRAKSFCKRLDIASGTAVRFEPG 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  urease (EC 3.5.1.5) 26K chain - Helicobacter felis
NyAlternate names: urease alpha chain
C.Species: Helicobacter felis
C.Species: 31-Dec-1993 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                    181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              red. No. 1.1e-39;
43; Mismatches 68.
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pybbby

pybbby

pybbby

pybbby

pybbby

pybbby

pybbble urease F12B7.10 (imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: Oz-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004

C;Accession: A95699

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Y; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

C.A.; Li, J.H.; Li, Y; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

A;Authors: Salzberg, S.L.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome l of the plant Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 SLDKFAETKEDNRIPGEILCEDECLTINIGRKAVILKVTSKGDRPIQVGSHYHFIEVNPY 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              155 LKFDREKAYGKRLDIPSGNTLRIGAGQTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHK 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFG-----
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                                                               A;Molecule type: protein
A;Residues: 1-246, R., 248-257, P., 259-268, S., 270-840 <TA2>
A;Cross-references: UNIPARC:UPI0000172D9F
K;Mamiya, G.; Takishima, K.; Masakuni, M.; Kayumi, T.; Ogawi
J. Protein Chem. 6, 55-59, 1987
                                                                                                                                                                                                                     A; Title: Complete amino acid sequence of jack bean urease. A; Reference number: A60883
                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-246, RV, 248-840 <TA3>
A;Cross-references: UNIPARC:UPI0000172D9E
R;Takishima, K.; Mamiya, G.
Protein Seq. Data Anal. 1, 103-106, 1987
A;Tile: Location of the essential cysteine residue of J
A;Reference number: S03364; MUID:88190054; PMID:3447159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.2%; Score 439.5; DB 1
39.6%; Pred. No. 1.7e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 39.6
Matches 99; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           240 AMHAVRSKGF 249
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         A;Reference number: JT0001
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                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
                                                                                                                                                                                                                                                                                  A; Accession: A60883
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 06-Jan-2003
C;Accession: D75586
C;Accession: D75586
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
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R;Takishima, K.; Suga, T.; Mamiya, G.
Bur. J. Biochem. 175, 151-165, 1988
A;Title: The structure of jack bean urease. The complete amino acid sequence, limited pr
                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPAKC:UPI0000D1CO5, GB:AE001863; GB:AE001825, NID:g6460670; PIDN:
A,Experimental source: strain R1
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C;Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          urease (EC 3.5.1.5) - jack bean
NyAlternate names: urea amidohydrolase
C;Species: Canavalia ensiformis (jack bean)
C;Species: Canavalia ensiformis (jack bean)
C;Date: 28-Dec-1987 #sequence revision 30-Sep-1993 #text change 05-Oct-2004
C;Accession: JC1396; S01021; JT0001; A60883; S03364; JS0642
R;Riddles, P.W.; Whan, V.; Blakeley, R.L.; Zerner, B.
Gene 121, 399-400, 1992
A;Reference number: JC1396; MUID:93077062; PMID:1446838
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A;Residues: 1-840 <RID>
A;Cross-references: UNIPROT:P07374; UNIPARC:UPI0000137DA7; GB:M65260
R;Riddles, P.W.; Whan, V.; Blakeley, R.L.; Zerner, B.
Gene 108, 265-267, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;; Score 483; DB 2; Length 228;
;; Pred. No. 8.6e-33;
44; Mismatches 70; Indels
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A,Residues: 1-246, R., 248-840 <TAL>
A,Cross-references: UNIPARC:UPION00172D9E
A,Memiya, G.; Takishima, K.; Masakuni, M.; Kayumi, T.; Ogar Proc. Upn. Acad B Phys. Biol. Sci. 61, 395-398, 1985
A,Title: Complete amino acid sequence of jack bean urease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 46.5%;
Matches 106; Conservative 4
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                                                                                                                                                                                                                                                                                  A, Accession: D75586
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-228 < WHI>
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Usease (EC 3.5.1.5) beta/gamma chain - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 06-Jan-2003
C;Accession: T29055
R;Redenbach, M.; Kieser, H.M.; Denapaite, D.; Eichner, A.; Cullum, J.; Kinashi, H.; Hopw Mol. Microbiol. 21, 77-96, 1996
A;Title: A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Si A;Reference number: 220556; MUID:97000351; PMID:8843436
A;Reference number: 220556; MUID:97000351; PMID:8843436
A;Reference number: 220556; Muid: GB/EMBL/DDBJ
A;Reference number: 220556; Muid: A;Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: ureAB
C;Superfamily: urease, fused gamma/beta subunit; urease 11K chain homology; urease 12K cl
C;Keywords: hydrolase
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A;Residues: 1-66,'K',68-100 <COL>
A;Cross-references: UNIPARC:UPI0000137D9A; EMBL:L07039; NID:g149330; PIDN:AAA25147.1; PI
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A, Residues: 1-100 <MUL>
A, Residues: 1-100 <MUL>
A, Cross-references: UNIPROT: P18316, UNIPARC: UP100001103C0, GB:M36068, NID:g149335, PIDN:
R, COLLIAN, C.M.; Gutman, D.M.; Laman, H.
Mol. Microbiol. 8, 187-198, 1993
A, Title: Identification of a nitrogen-regulated promoter controlling expression of Klebs
A, Reference number: S32937; MUID:93268094; PMID:8497192
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NiAlternate names: urea amidohydrolase; urease chain A; urease gamma chain
C;Species: Klebsiella pneumoniae
C;Species: Klebsiella pneumoniae
C;Species: A36.138, 532.938
R;Mulrooney, S.B.; Hausinger, R.P.
J. Bacteriol. 172, 5837-5843, 1990
A;Title: Sequence of the Klebsiella aerogenes urease genes and evidence for accessory | A, Reference number: A36138, MUID:91008957; PMID:2211515
61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                                                                                                                                                                            241 EIVDNLMKQGFM 252
                                                                                                                                            214 KALDKAKSHGFI 225
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A.Residues: 1-835 <MCD>
A.Cross-references: UNIRROT:000084; UNIPARC:UPI0000137DA9; EMBL:AL109820; PIDN:CAB52575.
C.Seberices: Strain 972h-; cosmid c1952
                                      A Status: preliminary
A Molecule type: DNA
A Molecu
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C;Species Schizosaccharomyces pombe
C;Species Schizosaccharomyces pombe
C;Dacession: T37939
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21755
A;Reference number: Z21755
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 419.5; DB 2
Pred. No. 7.7e-27;
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l Similarity 37.2%;
93; Conservative 5
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LMETMERRGF 249
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Best Local Similarity
    A; Accession: A96699
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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno A;Reference number: A99629; MUID:21156231; PMID:11258796
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A,Experimental source: strain O157:H7, substrain RIMD 0509952
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A;Cross-references: UNIPARC:UP10000D5DF7; GB:AE005174; NID:g12514462; PIDN:AAG55697.1;
A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                  A,Residues: 1-100 <STO>
A,Residues: 1-100 <STO>
A,Zross-references: UNIPROT:Q8XAG2; UNIPARC:UP100000D5DF7; GB:AE005174; NID:g12513945;
A,Experimental source: strain O157:H7, substrain EDL933
A,Accession: E85654
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C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004 C;Accession: B90794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 100;
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Best Local Similarity 57.0%
Matches 57; Conservative
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hes 57, Conservative
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A; Status: preliminary
                                                                                                                                                                                                                                                            A;Status: preliminary A;Molecule type: DNA
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                         A,Gene: ureA
C;Complex: trimer of heterotrimeric subunits consisting of 11K (gamma), 12K (beta), and
C;Complex: trimer of heterotrimeric subunits of one molecule of urea to carbon dioxide and tw
A;Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and tw
C;Superfamily: urease, gamma subunit; urease 11K chain homology
C;Keywords: heterotrimer; hydrolase; metalloprotein
F;1-100/Domain: urease 11K chain homology <UII>
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A;Cross-references: UNIPROT:P50043; UNIPARC:UPI0000137D9C; GB:Z83859; GB:AL123456; NID:g
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable ureA protein - Mycobacterium tuberculosis (strain H37RV)
C.Species: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C.Accession: H70664
C.Accession: Hamin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Gentles, S.; Hamin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
A.Authors: Sqares, R.; Sulston, J.B.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A.Attle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A.Accession: H70666
A.Accession: H70676
A.Accession: H70676
A.Accession: H70676
A.Accession: H70
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C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                            residues 1-100
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submitted to the Brookhaven Protein Data Bank, June 1995
A;Reference number: A65977; PDB:1KRA
A;Contents: annotation; X-ray crystallography, 2.3 angstroms, resid
R;Jabri, E.; Carr, M.B.; Hausinger, R.P.; Karplus, P.A.
Science 268, 998-1004, 1995
A;Title: The crystal structure of urease from Klebsiella aerogenes.
A;Title: The crystal structure of urease from Klebsiella aerogenes.
A;Reference number: A5640; MUID:92273988; PMID:7754395
A;Contents: annotation; X-ray crystallography, 2.3 angstroms
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C,Superfamily: urease, gamma subunit; urease 11K chain homology
F,1-100/Domain: urease 11K chain homology <U11>
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Pred. No. 1.7e-16;
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59.0%;
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Best Local Similarity 58.0%
Matches 58; Conservative
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Best Local Similarity 59.04
Matches 59; Conservative
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Search completed: November 28, 2005, 08:20:40 Job time : 15.5164 secs
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A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C; Accession: S74889
S; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystie
                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-100 «XAN»
A;Residues: 1-100 «XAN»
A;Cresidues: UNIPROT:P73796; UNIPARC:UP10000137DA2; EMBL:D90909; GB:AB001339; NIC
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Genetics:
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A;Cross-references: UNIPROT:P75030; UNIPARC:UP1000060B96; GB:299122; GB:AL009126; NID:9
A;Experimental source: strain 168
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C;Superfamily: urease, gamma subunit; urease 11K chain homology
F;1-100/Domain: urease 11K chain homology <U11>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: ureA
C;Superfamily: urease, gamma subunit; urease 11K chain homology
C;Keywords: hydrolase; metalloprotein
F;1-100/Domain: urease 11K chain homology <U11>
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                                                                                                                                                                                                                                                                                                                                          A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S74889
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C;Species: Bacillus sp.
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A36950
J. Bacteriol. 176, 432-442, 1994
A;Title: Cloning, sequencing, and expression of thermophilic Bacillus sp. strain TB-90 u. A;Accession: A36950
A;Atetus: preliminary
A;Aolecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Remidues: 1-100 cMAE>
A;Remidues: 1-100 cMAE>
A;Cross-references: UNIPROT:Q07399; UNIPARC:UPI0000137D95; GB:D14439; NID:g393296; PIDN:;C;Superfamily: urease, gamma subunit; urease 11K chain homology
C;Keywords: hydrolase
F;1-100/Domain: urease 11K chain homology <U11>
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N/Alternate names: ureA protein
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                                                                                                                      1 VKLTPKEQEKFLLYYAGEVA.....ADERHKHKALDKAKSHGFIK 226
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                                                                                                                     120 TLNAGKQATTLEVHNKGDRPVQVGSHFHFFEVNKLLEFDREKAYGKRLDIASGTAVRFEP 179
                                                                                                       61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKA-GEVKFGCDKDI 119
                                                                                                                                                       ELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGA 179
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"Molecular analysis of urease genes from a newly identified uncultured species of Helicobacter.";
species of Helicobacter.";
-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                       subunit family.
SIMILARITY: In the C-terminal section; belongs to the urease beta subunit family.
                                                          1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase alpha subunit)
                                   Gaps
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Helicobacteraceae, Helicobacter.
NCBI_TaxID=35817;
                                   5
           Length 234;
                                                                                                                                                                                                    GOTRKVOLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                    55; Indels
           Score 652; DB 1;
Pred. No. 9.4e-47;
  234 AA
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HAMAP, MF 00739; fused; 1.
InterPro; TPR002019; Urease_beta.
InterPro; IPR002026; Urease_gamma_reg.
InterPro; IPR008223; Urease_gamma_beta.
Pfam; PF00599; Urease_beta; 1.
Pfam; PF00599; Urease_beta; 1.
PIRSF; PIRSF001225; Urease_gammai.
ProDom; PD002326; Urease_beta; 1.
ProDom; PD002326; Urease_beta; 1.
TIGRFAMS; TIGR00192; urease_beta; 1.
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NUCLEOTIDE SEQUENCE (GENOMIC DNA).
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                                                                                                                                                                                                                                                                                                                                                                                                                              61 GRTLLKADDVMPGVAHMIHEVGIBAGFPDGTKLVTIHTPVBAGSDKLAPGEVILK-NEDI 119
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-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: In the N-terminal section; belongs to the urease gamma
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30-MAY-2000 (Rel. 39, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase alpha subunit).
Name=ureA; Synonyms=hpuA; OrderedLocusNames=JHP0068;
                                                                                                                                                                                                                                                                                                  1 MKLTPKELDKLMLHYAGELAKORKAKGIKLNYTEAVALISAHVMEEARAGKKSVADLMOE
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-!- SIMILARITY: In the C-terminal section; belongs to the urease beta
subunit family.
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MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;

Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown B.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genomic sequence comparison of two unrelated isolates of the human gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CAUTION: In Helicobacter the alpha subunit is what is known, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name-ureā, Synonyms-hpuā, OrderedLocusNames-JHP0068;
Helicobacter pylori 199 (Campylobacter pylori 199).
Bacteria, Proteobacteria, Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                              5
                                                                                                                              Length 234;
                                                                                                                                                                                              59; Indels
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180 GEEKTVELIDIGGNKRIYGFNALVDRQADHDGKKLALKRAKEKHF
   Urease gamma.
Urease beta.
CD5889E3D789C7F8 CRC64;
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                                                                                                                                                                                              41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001446; AAD05652.1; -; Genomic_DNA.
PIR; B71977; B71977.
                                                                                                                           52.7%; Score 622;
54.7%; Pred. No. 3
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HAMAP; MF 00739; fused; 1.
InterPro; IPR002019; Urease_beta.
102 Ur
234 Ur
25746 MW;
                                                                                                                                                             Best Local Similarity 54.79
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD:
   1 1
103 2
234 AA;
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Urease protein UreA.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Opazo P., Muller I., Rollan A., Valenzuela P., Yudelevich A.,
Garcia-de la Guarda R., Urra S., Venegas A.;
"Serological response to Helicobacter pylori recombinant antigens in
Chilean infected patients with duodenal ulcer, non-ulcer dyspepsia and
gastric cancer.",
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNOPEAIAYISAHIMDEARRGKKTVAQLMEE
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Muller I., Medina-Selby A., Palacios J.L., Martinez P., Opazo P.,
Muller I., Medina-Selby A., Palacios J.L., Martinez P., Opazo P.,
Bruce B., Mancilla M., Valenzuela P., Vudelevich A., Venegas A.;
Eloning and comparison of ten gene sequences of a Chilean H. pylori
strain with other H. pylori strains revealed higher variability for
VacA and CagA virulence factors.";
Biol. Res. 15:67-84(2002).
HSSP: PH479027; AAL86897.1; -; Genomic_DNA.
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                           51.9%; Score 613.5; DB 1; Length 238; 53.1%; Pred. No. 1.7e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                             238 AA; 26568 MW; A10B9DC4156C0561 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          42; Mismatches
InterPro; IPR002026; Urease_gamma_reg.
InterPro; IPR00823; Urease_gammabeta.
Pfam, PP00699; Urease_bera; 1.
Pfam, PP00547; Urease_gamma; 1.
PIRSF; PIRSF001225; Urease_gammabeta; 1.
ProDom; PD002326; Urease_bera; 1.
ProDom; PD002319; Urease_gamma; 1.
TIGRFAMS; TIGR0192; urease_bera; 1.
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GO; GO:0016151; F:nickel ion binding; IEA.
                                                                                                                                                                                                                                     Urease gamma
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MEDLINE=20123532; PubMed=10660136;
                                                                                                                                                                                                             Complete proteome; Hydrolase.
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 53.19
Matches 119; Conservative
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QBRNUS;
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                                                                                                                                                                                                                                                                                 SEQUENCE
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61 GRILLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CMHFLKKDEVMPGVGNMVPDLGVEATPPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VKLITPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                             51.8%; Score 611.5; DB 2; Length 238; 52.7%; Pred. No. 2.5e-43;
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GO; GO:0009039; F:urease activity; IEA.

GO; GO:0006807; P:nitrogen compound metabolism; IEA.

InterPro; IPR002013; Urease_beta.

InterPro; IPR002026; Urease_gamma_reg.

InterPro; IPR002026; Urease_gamma_reg.

Pfam; PF00699; Urease_gamma; 1.

Pfam; PF00699; Urease_gamma; 1.

ProDom; PD002125; Urease_gammabeta; 1.

ProDom; PD00219; Urease_gamma; 1.

RroDom; PD00219; Urease_gamma; 1.

IGRFAMS; TIGR00193; urease_beta; 1.

IGRFAMS; TIGR00193; urease_beta; 1.

SEQUENCE 238 AA; 26710 MW; E934A6512A559B28 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; PA373558; AAK69724.1; -; Genomic_DNA.
HSSP; P14916; 1E9Y.
SWR; Q93NJ1; 1-238.
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GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0009039; F:urease activity; IEA.
GO; GO:0006807; P:nitrogen compound metabolism; IEA.
InterPro; IPRO02019; Urease Beta.
InterPro; IPRO08223; Urease Gammabeta.
InterPro; IPRO08226; Urease Gamma reg.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 2.5e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62;
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Pfam: PF00547; Urease_gamma; 1.
PINSF: PINSF001225; Urease_gammabeta; 1.
ProDom; PD002316; Urease_beta; 1.
ProDom; PD002319; Urease_gamma; 1.
TIGRFAMS; TIGR00192; urease_gam; 1.
TIGRFAMS; TIGR00193; urease_gam; 1.
SEQUENCE 238 AA; 26672 NW; EE82BF861
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53.1%;
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Matches 118; Conservative
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MEDLINE=90264448; PubMed=2188975;
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                                                                                                                                                                                       61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                   LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                           Labigne A., Cussac V., Courcoux P., "Shuttle cloning and nucleotide sequences of Helicobacter pylori genes responsible for urease activity."; J. Bacteriol. 173:1920-1931(1991).
                                                          1 VKLIPKEQEKFLLYYAGEVARKRKAEGLKLNOPEAIAYISAHIMDEARRGKKTVAQLMEE
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01-APR-1992 (Rel. 22, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
13-SEP-2005 (Rel. 48, Last annotation update)
Name=ureA: Synonyms=hpuA; OrderedLocusNames=HP0073;
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MEDLINE=97394467; Pubmed-952185; DOI=10.1038/41483;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,

Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,

Peterson S.N., Loffus B.J., Richardson D.L., Dodson R.J., Khalak H.G.

Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,

Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,

Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,

Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,

Smith H.O., Fraser C.M., Venter J.C.;

"The complete genome sequence of the gastric pathogen Helicobacter
   Gaps
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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"The urease operon in Helicobacter pylori is regulated by decay of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
61; Indels
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[5]
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 AA
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 18:362-362(1990).
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Matches 119; Conservative
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UREA HELPY
UREA HELPY
UREA HELPY
DT 01-APR
DT 01-APR
DT 01-APR
DT 11-SEP
DE Urease
GN Helico
OC Bacter
OC 
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- MSCELLAMEDOUS: Oligomerization may protect the enzyme against denaturation in an acidic environment.
-!- SIMILARITY: In the N-terminal section; belongs to the urease gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        subunit family.
-!- SIMILARITY: In the C-terminal section; belongs to the urease beta
subunit family.
-!- CAUTION: In Helicobacter the alpha subunit is what is known, in
                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS), AND SUBUNIT STRUCTURE. MEDLINE=21267477; PubMed=11973617; DOI=10.1038/88635; HA N N-C., Oh S.-T., Sung J.Y., Cha K.A., Lee M.H., Oh B.-H.; Supramolecular assembly and acid resistance of Helicobacter pylori
                                                                                                                                      MEDLINE=90202165; PubMed=2318539;
Hu L.T., Mobley H.L.T.;
"Purification and N-terminal analysis of urease from Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Struct. Biol. 8:505-509(2001).
-1- CARALYITC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-1- SUBUNIT: Heterohexamer of 3 alpha and 3 beta subunits. Four heterohexamers assemble to form a 16 nm spherical complex.
G.I., Blaser M.J.;
urease from Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, X17079; CAA34932.1; -; Genomic_DNA.
EMBL, M60398; AAA25020.1; -; Genomic_DNA.
EMBL, A08816; CAA00810.1; -; Unassigned_DNA.
EMBL, AE001396; CAA00662.1; -; Unassigned_DNA.
EMBL, AE00129; AAD07144.1; -; Genomic_DNA.
EMBL, AB032429; BAA64532.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other bacteria as the beta subunit.
Dunn B.E., Campbell G.P., Perez-Perez "Purification and characterization of
                                                     pylori.";
J. Biol. Chem. 265:9464-9469(1990)
                                                                                                                                                                                                                                      Infect. Immun. 58:992-998(1990).
                                                                                                                   PROTEIN SEQUENCE OF 1-20
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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                GO: GO: 0005737; C: Cytoplasm; IEA.
GO: GO: 0005737; C: Cytoplasm; IEA.
GO: GO: 00016151; F: nickel ion binding; IEA.
GO: GO: 0006807; F: nitrogen compound metabolism; IEA.
InterPro; IPR002019; Urease_Jenmabeta.
InterPro; IPR002026; Urease_gammabeta.
InterPro; IPR002026; Urease_gammabeta.
InterPro; IPR005026; Urease_gamma_reg.
Pfam; PF00599; Urease_Bamma; 1.
PIRSF; PIRSF001225; Urease_gammabeta; 1.
ProDom; PD002319; Urease_gammabeta; 1.
ProDom; PD002319; Urease_gamma; 1.
ITGRPAMs; ITGR00192; urease_beta; 1.
ITGRPAMs; ITGR00193; urease_gam; 1.
SEQUENCE 238 AA; 26586 MW; DFDBA17D016FC351 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.7%; Score 610.5; DB 2; Length 53.1%; Pred. No. 3e-43; artive 42; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chu C., Ou J.T.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMR; Q33NI5; 1-238.
GO; GO:0005737; C:Cytoplasm; IEA.
GO; GO:0005737; C:Cytoplasm; IEA.
GO; GO:0005737; C:Cytoplasm; IEA.
GO; GO:0006807; F:nitrogen compound metabolism; IEA.
GO; GO:0006807; F:nitrogen compound metabolism; IEA.
InterPro; IPR002019; Urease_gammabbta.
InterPro; IPR002019; Urease_gamma_reg.
InterPro; IPR002025; Urease_gamma_reg.
From; PF00699; Urease_beta; 1.
Propom; PD002326; Urease_beta; 1.
Propom; PD002326; Urease_beta; 1.
Propom; PD002326; Urease_beta; 1.
Propom; PD002319; Urease_beta; 1.
TIGRFAMS; TIGR00192; urease_beta; 1.
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Last sequence update)
Last annotation update)
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HSSP; P14916; 1E9Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q93NIS HELPY PRELIMINARY;
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NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Name=ureA;
Helicobacter pylori (Campylobacter pylori).
Helicobacteraceae; Froteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacteria;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF373570; AAK69736.1; -; Genomic_DNA.
HSSP; P14916; IESY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26540 MW; 4E77328669CD9A2D CRC64;
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rive 43; Mismatches
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Q93NI3;
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  NUCLEOTIDE SEQUENCE.
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InterPro; IPR002019; Urease beta.
InterPro; IPR008223; Urease_gammabeta.
InterPro; IPR002026; Urease_gamma_reg.
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Helicobacteraceae, Helicobacter
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Matches 118; Conservative
                                                                                                        Q933M9 HELPY PRELIMINARY;
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Q932S5;
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AC 0932S
DT 01-DE
DT 01-FE
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GN Name=
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                                                               1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                Gaps
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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    Length 238;
                                                                                                                                                                                                                                                                       Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR373562; AAK69728.1; -; Genomic_DNA.
HSSP; P14916; 1E9Y.
SMR; Q93NI8; 1-238.
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GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0009039; F:ureae activity; IEA.
GO; GO:0006807; P:nitrogen compound metabolism; IEA.
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Last annotation update)
    DB 2;
                                62;
51.7%; Score 610.5; DB 52.7%; Pred. No. 3e-43; tive 43; Mismatches 6
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PIRSF; PIRSF001225; Urease_gammabeta; 1.
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InterPro; IPR008223; Urease_gammabeta.
InterPro; IPR002026; Urease_gamma_reg.
Pfam; PF00699; Urease_beta; 1.
Pfam; PF00547; Urease_gamma; 1.
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ProDom; PD002319; Urease_gamma; 1.
TIGRFAMS; TIGR00192; urease_bera; 1.
TIGRFAMS; TIGR00193; urease_gam; 1.
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                                Matches 118; Conservative
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Best Local Similarity
                Similarity
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SEOUENCE
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    Query Match
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.5%; Score 608.5; DB 2; Length 238; 52.7%; Pred. No. 4.5e-43; ive 43; Mismatches 62; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chu C., Ou J.T.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64A0C32A043A8BD8 CRC64;
                             181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005/37; C:cytoplasm; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0009039; F:urease activity; IEA.
GO; GO:0006807; P:nitrogen compound metabolism; IEA.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                Last annotation update)
                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                      238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF373580; AAK69746.1; -; Genomic DNA.
EMBL; AF373572; AAK69738.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00699; Urease Deta; 1.
Pfam; PF00699; Urease Jamma, 1.
PIRSF; PRSF001225; Urease gammabeta; 1.
ProDom; PD002326; Urease Deta; 1.
ProDom; PD002319; Urease Deta; 1.
TIGREAMS; TIGR00192; urease Deta; 1.
TIGREAMS; TIGR00193; urease gam; 1.
SEQUENCE 238 AA; 26599 MW; 64A0C32A0
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Best Local Similarity 52.28
Matches 117; Conservative
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Q93NJO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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DT 01-DEC-2
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OC BACTERIA PICODA
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셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 INAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKLTPKELDKLMLHYAGELARKRKEKGIKLNYVEAVALISAHIMEBARAGKKSAAELMOE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                            Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales, Helicobacteraceae, Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : : |: || : || :::: | | || || || EKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chu C., Ou J.T.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR313569; AAK69735.1; -; Genomic_DNA.
HSSP; P14916; 1B9Y.
SMR; Q93N14; 1-238.
                                                                                                                                                                                                                                                                (APR-2001) to the EMBL/GenBank/DDBJ databases
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DAR-2004 (TrEMBLrel. 26, Last annotation update)
Urease protein UreA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.4%; Score 607.5; DB 2; 52.7%; Pred. No. 5.4e-43; iive 43; Mismatches 62;
                                                                                                                                                                                                                                                                            EMBL; AF373584; AAK69750.1; -; Genomic_DNA. EMBL; AF373559; AAK69723.1; -; Genomic_DNA. EMBL; AF373559; AAK69723.1; -; Genomic_DNA. EMBL; AF373559; AAK69725.1; -; Genomic_DNA. EMBL; AF373581; AAK69747.1; -; Genomic_DNA. EMBL; AF373582; AAK69749.1; -; Genomic_DNA. EMBL; AF373582; AAK69748.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 AA
Helicobacter pylori (Campylobacter pylori)
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Q93NI4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
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                                                                                                        NCBI_TaxID=210;
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Submitted (
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093NI4 HELL
1D 059NI
AC 093NI
AC 093NI
DT 01-DE
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61 GRSLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFFANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2; Length 238;
GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:000533; F:unickel ion binding; IEA.

GO; GO:0006803; F:unicxel ion binding; IEA.

GO; GO:0006807; F:unitrogen compound metabolism; IEA.

InterPro; IPRO02019; Urease_Deta.

InterPro; IPRO02026; Urease_Gammabeta.

InterPro; IPRO50205; Urease_Gammabeta.

Pfam; PPO0699; Urease_Beta; I.

PFEM; PRO5047; Urease_Gammabeta; I.

PFISF; PIRSF001225; Urease_Gammabeta; I.

ProDom; PD002319; Urease_Beta; I.

ProDom; PD002319; Urease_Beta; I.

RTGRFAMS; TIGR00193; urease_beta; I.

RTGRFAMS; TIGR00193; urease_Beta; I.

SEQUENCE 238 AA; 26511 MW; CA6677D2788BDD2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
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52.2%; Pred; No. 5.4e-43;
"...matches 62; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF773560; AAK69726.1; -; Genomic_DNA.
HSSP; P14916, 1E9Y.
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GO; GO:0005737; C:cytoplasm; IEA.

GO; GO:0016151; F:nickel ion binding; IEA.

GO; GO:0009039; F:urease activity; IEA.

GO; GO:0006807; P:nitrogen compound metabolism; IEA.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Urease protein UreA.
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InterPro; IPR002025; Urease_gammabeta.
InterPro; IPR002025; Urease_gammabeta.
InterPro; IPR002026; Urease_gammareg.
Pfam; PF00547; Urease_gamma; 1.
Pr05m; PF005326; Urease_gammabeta; 1.
Pr05m; PD002326; Urease_Beta; 1.
Pr05m; PD002319; Urease_gamma; 1.
ITGRFAMS; TIGR00193; urease_gamm; 1.
SEQUENCE 238 AA; 26629 WW; 5C082660A
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Search completed: November 28, 2005, 08:19:44 Job time : 88.8136 secs
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                                                                                                                                                                                                                                                                                                   LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                               61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                                                                                                                                                                  61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                               1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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  51.4%; Score 607.5; DB 2; Length 238; 52.7%; Pred. No. 5.4e-43; ive 43; Mismatches 62; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Churchild Servence.

Churchild (APR-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AR373556; AAK69722.1; -; Genomic_DNA.

EMBL; AR373556; AAK69722.1; -; Genomic_DNA.

EMBL; AR373556; AAK69722.1; -; Genomic_DNA.

SMR; Q3NJZ; 1-238.

GO; GO:0005737; C:Cytoplasm; IEA.

GO; GO:0009039; Furease activity; IEA.

GO; GO:0009039; Furease beta.

InterPro; IPR002026; Urease_Jammabeta.

R InterPro; IPR002026; Urease_Jammabeta.

R InterPro; IPR002026; Urease_Jammabeta.

R Pfam; PF00694; Urease_Jammabeta; 1.

Probom; PD002316; Urease_Jammabeta; 1.

Probom; PD002316; Urease_Jammabeta; 1.

R Probom; PD002316; Urease_Jamma, 1.

R TIGRFAMS; TIGR00192; urease_beta; 1.

TIGRRAMS; TIGR00193; urease_beta; 1.

R TIGRFAMS; TIGR00193; urease_Bam; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 AA
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Q93NJ2;
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Matches 118; Conservative
                            Best Local Similarity 52.79
Matches 118; Conservative
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NUCLEOTIDE SEQUENCE.
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Query Match
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C933NJ2 HELL
LD Q933NJ
AC Q93NJ2
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DT 01-DE
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61 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
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                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter. NCBI _TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.3%; Score 605.5; DB 2; Length 238; 52.7%; Pred. No. 8e-43; tive 42; Mismatches 63; Indels 1;
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224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Iran-HP031;

Karimi Arzenani M., Mohammadi M.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY227442; AA034402.1; -; Genomic_DNA.
HSSP; P14916; 1E9Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 AA; 26491 MW; 6384770531FCB38C CRC64;
181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                SNR, Q84F76; 1-238.

GO; GO: 0005737; C: Cytoplasm; IEA.
GO; GO: 0016737; F: Ptydrolase activity; IEA.
GO; GO: 0016151; F: nickel ion binding; IEA.
GO; GO: 0009039; F: urease activity; IEA.
GO; GO: 0009039; F: urease activity; IEA.
GO; GO: 0008030; P: urease beta:
InterPro; IPR008223; Urease Deta:
InterPro; IPR008223; Urease Gammabeta.
InterPro; IPR0082026; Urease Gamma reg.
                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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Pfam; PF00547; Urease_gamma; 1.
PIRSF; PIRSF001225; Urease_gammabeta; 1.
ProDom; PD002326; Urease_beta; 1.
ProDom; PD002319; Urease_gamma; 1.
TIGRFAMS; TIGR00192; urease_beta; 1.
                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                      Urease alpha (EC 3.5.1.5).
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Matches 118; Conservative
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Q84F76;
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Adj88250 UreaseXY
Adj88241 UreaseXY
Adj88247 UreaseXY
Adj58244 UreaseXY
Add37849 H. bizzoz
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H. pylori
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                                                                                                                                                                                                                                                                                                 VKLTPKEQEKFLLYYAGEVA......ADERHKHKALDKAKSHGFIK 226
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Aaw07193 |
Aau35693 |
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                          2443163 seqs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                November 28, 2005, 07:55:02
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Maximum Match 100%
Listing first 45 summaries
                                                                                                  using sw model
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geneseqp2002s:*
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Gapop 10.0 , Gapext
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Maximum DB seq length: 200000000
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Match Length DB
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1: geneseqp198
                                                                                               - protein search,
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Perfect
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Aam49648		3 Abu42523 Protein	0 Abu41210 Protein	2 Aau33952 Staphyloc	5 Abu20285 Protein	7 Abu40327 Protein	3 Abu27583 Protein		3 Abu22153 Protein	6 Aar67376 P. mirabi	Aaw14497	Adj66032	D Aea54210	1 Abu50981 Helicobac	7 Aar67377 Canavalia	Adg65522 (	5 Aaw37775 Klebsiel	3 Aay81823 Klebsiel	Aau36152 Klebsiel	6 Abu32326 Protein e
AAM49648	ABU42650	ABU42523	ABU41210	AAU33952	ABU20285	ABU40327	ABU27583	ABU17114	ABU22153	AAR67376	AAW14497	ADJ66032	AEA54210	ABU50981	AAR67377	ADG65522	AAW37775	AAY81823	AAU36152	ABU32326
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47	42.	42	41.	41.4	40.	39.	39.	39.	38	38.	37.	37.2	37.	37.0	36.	31.2	23.	23.	23.8	23.
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559	502.5	497.5	493	489.5	477	470.5	470	469	455.5	449	443	439.5	439.	437	429.5	368	281.5	281	281	281
22	56	27	58	59	30	31	32	33	34	35	36	3.7	38	39	40	41	42	43	44	45

## ALIGNMENTS

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The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis in Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an urease X subunit polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of
                                                                                                                                   immunogenic fragment; antibacterial; Vaccine; Helicobacter felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID NO 2; 76pp; English
            ADJ58238 standard; protein; 226 AA
                                                                                                        Urease subunit polypeptide X.
                                                                                                                                                                                                                                                                11-JUL-2001; 2001EP-00202666.
                                                                                                                                                                                                                                                                                             17-JUL-2000; 2000EP-00202565.
                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                          Cattoli G,
                                                                                                                                                                                                                                                                                                                            (ALKU ) AKZO NOBEL NV
                                                                                                                                                                                                                                                                                                                                                                                         2002-124384/17.
                                                                                                                                                                      Helicobacter felis.
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                                                                         06-MAY-2004
                                                                                                                                                                                                                                  30-JAN-2002
                                            ADJ58238
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ADJ58238
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Sequence 226 AA;

Query Match

100.0%; Score 1181; DB 5; Length 226;

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Matches
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                                                                               CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                           CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                       LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                  LINAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of vaccines.
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                                                   VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                      VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                    Gaps
                                                                                                                                                                                                                                                                                                                       antibacterial; Vaccine; Helicobacter felis.
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                                                                                                                                                               QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGFIK 226
                   Indels
                                                                                                                                                                          OTRKVQLI PLGGSKKVI GMNGLVNN I ADERHKHKALDKAKSHGFIK
         Pred. No. 6.8e-116;
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                  Mismatches
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Pred. No. 1.
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                                                                                                                                                                                                                                      ADJ58250 standard; protein; 226 AA
100.08; P1.
                                                                                                                                                                                                                                                                                                                                                                                                       11-JUL-2001; 2001EP-00202666.
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                                                                                                                                                                                                                                                                              (first entry)
        Best Local Similarity 100.
Matches 226; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cattoli G;
                                                                                                                                                                                                                                                                                                                        immunogenic fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                               (ALKU ) AKZO NOBEL NV.
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                                                                                 121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG
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CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE
                                                 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDI PSGNTLRIGAG
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nes 224;
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VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE

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RESULT 5
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CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIBPDEHFKAGEVKFGCDKDIE 120
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Pred. No. 3.7e-115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAELMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CMHPLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWP1EPDEHFKAGEVKFGCDKD1E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                           antibacterial; Vaccine; Helicobacter felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTRKVOLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGFIK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGFIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1170; DB >,
No. 9.8e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 9.8e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 8; 76pp; English
ADJ58244 standard; protein; 226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ37849 standard; protein; 234 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.1%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                           11-JUL-2001; 2001EP-00202666.
                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JUL-2000; 2000EP-00202565
                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                             immunogenic fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ALKU ) AKZO NOBEL NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cattoli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-124384/17.
                                                                                                 (first
                                                                                                                                              UreaseXY subunit #3
                                                                                                                                                                                                                                             Helicobacter felis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
ses 223; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADJ58243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 226 AA;
                                                                                                                                                                                                                                                                                                                                            30-JAN-2002
                                                                                                 06-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kusters JG,
                                                 ADJ58244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
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180 GOTRKVOLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 

ò 셤 prokaryotic cellular proliferation protein; antibiotic;

antibacterial; drug design.

Helicobacter pylori

NO200170955-A2

27-SEP-2001

Helicobacter pylori cellular proliferation protein #188

14-FEB-2002 (first entry)

AAU35875 standard; protein; 238 AA

AAU35875

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Novel isolated nucleic acid molecule having urease gene cluster, and conferring on Helicobacter bizzozeronii ability to produce urease, useful as vaccine for preventing disease in mammals infected by H.bizzozeronii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKA-GEVKFGCDKDI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKLTPKELDKLMLHYAGELAKKKKANGVKLNYTEAVALISAHVMEEARAGKKSVADLMQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                               Urease, urease gene cluster; urease structural gene; urease accessory gene; ureA; Helicobacter bizzozeronii infection; antibacterial; enzyme.
                                                                                                                                                                                                                                                                                                                                                          Claim 23; SEQ ID NO 3; 40pp; English.
                                          H. bizzozeronii ureA polypeptide.
                                                                                                                                                                                                                                                             Zhu J;
                                                                                                                                                                        12-AUG-2003; 2003US-00639273
                                                                                                                                                                                             16-AUG-2002; 2002US-0404337P
                     (first entry)
                                                                                                          Helicobacter bizzozeronii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 57.3
Matches 129; Conservative
                                                                                                                                                                                                                                                             Chang Y, Simpson KW,
                                                                                                                                                                                                                 (CHAN/) CHANG Y.
(SIMP/) SIMPSON K W.
                                                                                                                                                                                                                                                                                 2004-533502/51.
                                                                                                                                                                                                                                                                                WPI; 2004-533502/
N-PSDB; ADQ37848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 234 AA;
                                                                                                                              US2004142343-A1
                                                                                                                                                                                                                                      (ZHUJ/) ZHU J.
                     07-0CT-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptide.
                                                                                                                                                  22-JUL-2004.
 ADQ37849;
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셤
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Carr GJ;

Trawick JD,

Wall D,

Ohlsen KL, Zyskind JW, Xu HH;

WPI; 2001-611495/70.

N-PSDB; AAS53734.

2000US-0191078P. 2000US-0206848P. 2000US-0207727P. 2000US-0242578P. 2000US-0253625P.

2001US-0269308P

27-NOV-2000; 22-DEC-2000; 16-FEB-2001;

23-OCT-2000;

(ELIT-) ELITRA PHARM INC

Haselbeck R,

Yamamoto RT,

21-MAR-2001; 2001WO-US009180

21-MAR-2000; 23-MAY-2000; 26-MAY-2000;

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The invention relates to an isolated nucleic acid molecule conferring on Helicobacter bizzozeronii an ability to produce urease, where the nucleic acid molecule is a urease gene cluster comprising at least one urease extructural gene and at least one urease accessory gene. The nucleic acid molecule is chosen from ureA, ureB, ureE, ureG, ureH and ureI. The invention also relates to an isolated protein encoded by the nucleic acid, a vaccine for preventing onstead protein encoded by the nucleic acid, a vaccine for preventing a nucleic acid and a carrier, and an isolated attibody or its binding portion raised against the nucleic acid. The nucleic acids, proteins and antibodies are useful for vaccinating mammals against onset of disease caused by infection of H. bizzozeronii, which involves administering the sequences. The sequences are useful for detecting H. bizzozeronii in a sample of tissue or body fluids which involves providing a nucleotide sequence as a probe in a nucleic acid and detecting any reaction which indicates that H. bizzozeronii is present in the sample. This sequence represents the H. bizzozeronii ureA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.2%; Score 652; DB 8; Length 234; 57.3%; Pred. No. 5e-60; ive 39; Mismatches 55; Indels
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prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonla typhi, Klebsiella pneumoniae, Beeudomonae aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to identify proteins used in proliferation, to express these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense mucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to antisense inhibitors of genes essential to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51.9%; Score 613.5; DB 53.1%; Pred. No. 6e-56; ive 42; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 3; SEQ ID NO 11468; 511pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 119; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 238 AA;
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120 TLNAGKQATTLEVHNKGDRPVQVGSHPHFFEVNKLLEFDREKAYGKRLDIASGTAVRFEP 179

120 ELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGA 179

61 GRTLLKADDVMPGVAHMIHEVGIEANPPDGTXLVTIHTPVEDGGHKLAPGEVILK-NEDI

q ò g

g ò 셤 8 셤 ò 셤

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Urease A (AAW07193) and B (AAW07194) subunits of Helicobacter pylori are encoded by the ureA + ureB gene locus of clinical isolate CPM630.
Vectors, e.g. pORV214 (see also AAT44351), carrying the gene locus can be used to transform host cells for the large-scale prodn. of recombinant, enzymatically inactive, multimeric urease. The urease complex induces a mucosal immune response that can treat or prevent Helicobacter, esp. H.
pylori, gastroduodenal infection. (Updated on 16-OCT-2003 to standardise
                    Vaccine for inducing mucosal response to Helicobacter - contg. multimeric urease complex and pref. an antibiotic, anti-secretory agent or bismuth
LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRITLIKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kleanthous H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.7%; Score 610.5; DB 2; Length 238; 52.7%; Pred. No. 1.2e-55; ive 43; Mismatches 62; Indels 1;
                                                                                     224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soman G,
Bhagat H,
                                                                                                              QTRKVOLI PLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Thomas WD,
Guirakhoo F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 70-71; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Urease; ureA gene; ureB gene; vaccine
                                                                                                                                                                                                                                               Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori; strain CPM630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ackerman SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ermak T,
                                                                                                                                                                                                                                            AAW07193 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96WO-US005800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-00431041
95US-00568122
                                                                                                                                                                                                                                                                                                                                                                                                 H. pylori urease A subunit.
                                                                                                                                                                                                                                                                                                                                (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 52.79
Matches 118, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weltzin RA, Pappo J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-497373/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ORAV-) ORAVAX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Monath TP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAT44351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9633732-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-APR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-APR-1995;
06-DEC-1995;
                                                                                                                                                                                                                                                                                                                                16-OCT-2003
11-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-OCT-1996
    121
                                                                                                                                                                                                                                                                                       AAW07193;
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                                                                                          181
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OS field
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     salt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lee
                                                                                                                                                                                                                          AAW07193
                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                   셤
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                                                                                              GRILLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                    The protein can be used for the prodn. of antibodies and to prepare vaccines for the prevention /treatment of C. pylori infections. See also AAR04578-81. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRILLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                   CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                         121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleotide sequences encoding Campylobacter pylori-ureaseents - and derived vectors, transformants, protein, antibodies and probes, useful idiagnosis, treatment and prevention of infections.
1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 238;
                                                                                                                                                                                                                                                                       EEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF 223
                                                                                                                                                                                                                                               QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 610.5; DB 2
Pred. No. 1.2e-55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INSP ) INST PASTEUR.
(INRM ) INSERM INST NAT SANTE & RECH MED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Part of protein with urease activity.
                                                                                                                                                                                                                                                                                                                                                                                                      Ź
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 34; 47pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                 AAR04579 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.7%;
52.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1990-147844/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAQ04328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 238 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Urease; probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-AUG-2003
25-MAR-2003
21-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9004030-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Labigne A;
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR04579;
                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                         180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                      ARESULT 8

AAR04579

AAR04579

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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, pseudomonas aeruginosa and Enterococcus faccalis. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify antibodies capable of binding to the express these proteins. The proteins antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an essential prokaryotic cellular proliferation protein. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in celectronic format directly from WINDO at the wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antisense; prokaryotic cellular proliferation protein; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              성
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohlsen KL, Zyskind JW, Wall D, Trawick JD,
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids.
                                  EEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori cellular proliferation protein #6.
   QTRKVOLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 3; SEQ ID NO 11286; 511pp; English.
                                                                                                                                                                                                                              AAU35693 standard; protein; 238 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-0206848P.
2000US-0207727P.
2000US-0242578P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2001; 2001WO-US009180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0191078P
                                                                                                                                                                                                                                                                                                                                                                 14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-611495/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAS53552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Haselbeck R,
Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-NOV-2000;
22-DEC-2000;
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26-MAY-2000;
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                                                             180
                                                                                                                                                                                                                                                                                                AAU35693;
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This invention describes a novel method for the preparation of a vaccine based on T cell-stimulating peptide sequences. The method comprises (1) identifying potential Mic (major histocompatibility complex)-binding and T cell-reactive epitopes in a target protein; (2) eliminating cross-reactive epitopes, and (3) verifying remaining epitopes by determining their activity in vitro and/or in vivo. The products of the invention have antibacterial, antiulcer, antinflammatory, cytostatic, virucide, protozoacide and immunosuppressive activity. The vaccine is especially used to protect against infection by Helicobacter pylori, but more generally can be prepared from proteins from any pathogen (virus, bacterium, protozoan) or tumour, or associated with autoimmune disease. Synthetic epitopes that are more immunogenic than natural sequences can be identified, and the vaccine may have increased immunogenicity (when formulated with adjuvant) or immunotolerance (formulated without an adjuvant). This sequence represents the urease A protein PA4 described in
                                                                                                 61 GRILLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                              Urease A; vaccine; T cell-stimulating peptide; antibacterial; antiulcer; MHC; major histocompatibility complex; epitope; antiinflammatory; cytostatic; virucide; protozoacide; immunosuppressive; pathogen; tumour; autoimmune disease; Helicobacter pylori infection.
Preparing vaccine containing T cell-stimulating peptides, useful particularly for protection against Helicobacter pylori, by selecting epitopes from target proteins.
                                                                               61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE
                                                                                                                                                       121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG
                                                                                                                                                                                                                                                                        223
                                                                                                                                                                                                                                  181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                        180 EEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meyer TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lucas B,
                                                                                                                                                                                                                                                                                                                                                                     AAM49644 standard; protein; 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 3; 36pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-JUL-2001; 2001WO-EP007656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2000; 2000DE-01032538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bumann D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Urease A protein PA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-164497/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 238 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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                                                                                                                                                                                                                                                                                                                                 RESULT 11
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51.7%; Score 610.5; DB 4; Length 238; 52.7%; Pred. No. 1.2e-55; ive 43; Mismatches 62; Indels 1.

Best Local Similarity 52.7 Matches 118; Conservative

Query Match

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The invention relates to inducing an immune response against Helicobacter in a mammal, comprising mucosally administering to the mammal an attenuated Salmonella vector containing a nucleic acid molecule encoding a Helicobacter antigen, and parenterally administering to the mammal a Helicobacter antigen, and parenterally administering to the mammal a Helicobacter antigen. Also included is an attenuated Salmonella vector comprising a nucleic acid molecule encoding a Helicobacter antigen. The Helicobacter antigen is a urease, a urease subunit, or its immunogenic fragment (encoded by the urea and urea genes). The mammal is at risk of having but does not have Helicobacter infection or has a Helicobacter infection. The attenuated Salmonella vector further comprises an htra or nirB promoter. The vector can be used in inducing an immune response against Helicobacter in a mammal. The vector can be used to treat Helicobacter infection. The vector and the method can be used to treat
                                                                                                                                                       61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                         LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                    1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                      1 MKLTPKELDKIMIHYAGELAKKRKEKGIKINYVEAVALISAHIMEEARAGKKTAAELMOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mammals, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DHUR3; vaccine; helicobacter pylori infection; urease; immune stimulation; antibacterial; Immunostimulant; antiulcer; cytostatic; antinflammatory; gastrointestinal-gen.; gastritis;
                                     ;
Length 238;
                                                                                                                                                                                                                                                                          181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                 Inducing an immune response against Helicobacter in ma
treating Helicobacter induced gastroduodenal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hylicobacter pylori Urase A protein fragment SEQ ID
 DB 5;
                                   62:
                   . 2e-55;
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 51.7%; Score 610.5; 52.7%; Pred. No. 1.2e
                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               AEB55115 standard; protein; 245 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kleanthous H, Londono-Arcila P,
                                   43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-2000; 2000WO-US030191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-00431705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ulcer; carcinoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Helicobacter pylori.
Salmonella typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-343379/36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ORAV-) ORAVAX INC
                   Similarity
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               Best Local Simi
Matches 118;
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                                                                                                                                                                                                         121
   Query Match
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Helicobacter induced gastroduodenal diseases, including acute, chronic or

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atrophic gastritis, peptic ulcer diseases (e.g. gastric or duodenal ulcers), and gastric carcinoma. Attenuated Salmonella vector pHUR3 was constructed expressing UreA and UreB and including an E. coli AmpR gene. The present sequence represents a protein or peptide encoded by the pHUR3 plasmid. NOTE: pHUR3 is represented by both ABB5512 and ABB55130, the peptides expressed by pHUR3 are shown in the sequence listing to be split between ABB55112 and ABB55130, yet Figure 4 shows all the peptides being expressed by the one sequence, therefore all encoded peptides are cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a protein having a specific region of primary structure of the beta-subunit Helicobacter pylori urease, appearing as ADS09176 (amino acids 201-318 of the beta subunit) or a sequence which generates antibodies that suppresses proliferation of H. pylori and which suppresses urease activity of H. pylori by an immune reaction. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein having specific region of beta-subunit urease of Helicobacter pylori, which generates antibodies that suppress proliferation and urease activity of bacteria, useful for preventing Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                        180
                                                                                                                                                                                                                                                                                                                                                                                                                                              CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                    67
                                                                                                                                                                                                                                                                                                     LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG
                                                                                                                                                                                                                                                                                     1 VKLIPKEQEKFLLYYAGEVARKRKAEGLKLNQPBAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Urease, alpha subunit, UreB, gastric ulcer, peptic ulcer, gastritis, stomach cancer, vaccine, antibody, immune reaction.
                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                 Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : : |:|| : || : || : | : | | || || || EEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                 4.
                                                                                                                                                                                                                                                   62;
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FUKUYAMA RINSHO KENSA CENT KK.
                                                                                                                                                                                                               ; Score 610.5; DB 4; Pred. No. 1.3e-55; 43; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 3; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H. pylori urease alpha beta subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADS09178 standard; protein; 238
                                                                                                                                                                                                                 51.7%;
52.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-FEB-2003; 2003JP-00054654.
                                                                                                                                              referenced to both sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                 Query Match
Best Local Similarity 52.77
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-665475/65
                                                                                                                                                                              Sequence 245 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   187
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vaccine against H. pylori. The present invention describes generating monoclonal antibodies against the urease using hybridoma techniques that are useful for passive immunisation and diagnostic techniques. Furthermore, the antibacterial peptide can be used to immunise an animal in order to produce antibodies that are present within a functional food such as milk or eggs. This polypoptide sequence is the H. pylori urease alpha subunit protein of the invention.

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inducing an antibody response, such that it can be used to develop a

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H. pylori comprising the urease fragment, a transformed cell transformed by introducing the gene, an antibody which recognises the urease fragment and transforming a plant by introducing the gene into the plant and making it express. The urease fragment is useful for producing blood serum containing antibodies which suppresses proliferation of H. pylori and which suppresses urease activity of H. pylori which involves immunising a living organism (e.g. a human, cow or hen) with the urease fragment. The fragment may be purified from cow's milk or hen eggs from transgenic animals expressing the fragment. H. pylori is thought to be a cause of gastric and peptic ulcers, gastritis and may be implicated in stomach cancer. The urease enzyme is thought to be responsible for maintaining the bacterium in the acid conditions of the stomach. The present sequence is the H. pylori urease alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                               GRILLKPDDVMDGVASMIHEVGIBAMFPDGTKLVTVHTFIBANGKLVPGEL-FLKNEDIT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                              1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE 60
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 included are a gene which encodes the urease fragment, a vaccine against
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                              51.4%; Score 607.5; DB 8; Length 238; 52.2%; Pred. No. 2.6e-55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori urease alpha subunit protein SeqID 2.
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                                                                                                                                                                                                                                                                                                                Matches 117; Conservative
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1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE

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63; DB 8;

51.1%; Score 603.5; DB 8 52.2%; Pred. No. 6.8e-55; iive 43; Mismatches 63

Best Local Similarity 52.2% Matches 117; Conservative

Query Match

Sequence 238 AA;

Length 238; Indels 유

121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG

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The sequence of the Helicobacter felis urease ureA gene product (given in AAR67311) was compared to ureases of Helicobacter pylori (AAR67375), Proteus mirabilis (AAR67376) and jack bean urease (AAR67377) and regions of homology were identified. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA from Helicobacter pylori and Helicobacter felis - used to develop prods. for detection, treatment and prevention of Helicobacter infection
                                                                                                                                                                                              Jrease; ureA gene; immunogen; vaccine; diagnostic; Helicobacter felis.
            OTRKVOLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Fig 41-iii, 168pp, English.
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(INRM ) INST NAT SANTE & RECH MEDICALE
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93WO-EP003259
                                                                                                                                   (revised)
(first entry)
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                                                                                                                                                                       H. pylori ureA urease.
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                                                                                                                                                                                                                      Proteus mirabilis.
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19-NOV-1993;
                                                                                                                                  25-MAR-2003
22-JUN-1995
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This invention relates to a novel immunogenic peptide that induces production of antibodies against the Helicobacter pylori (H. pylori) urease protein. Specifically, it refers to a peptide antigen capable of

New peptide useful as a vaccine against Helicobacter pylori induces an antibody response against the bacterial urease.

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN

WPI; 2004-162021/16.

Disclosure; SEQ ID NO 2; 19pp; Japanese.

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		1;
		Gaps
	238;	
	Length	Indels
	DB 2;	63;
	Query Match 51.0%; Score 602.5; DB 2; Length 238; Bost Local Similarity 52.2%; Dred No. 8 7a-55.	13; Mismatches
	51.0%;	vative 4
8 AA;	ilarity	Conser
nce 23	tch	117;
SQ Sequence 238 AA;	sery Ma	atches
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<sup>61</sup> GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVFGEL-FLKNEDIT 119
121 LNACKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
120 INEGKKAVSVKVKNVGDRFVQIGSHFHFFEVNRCLDFDREKTFHKRLDIASGTAVRFEFG 179

Search completed: November 28, 2005, 08:14:34 Job time : 76.7204 secs

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Sequence 15, Appl
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Sequence 70574, A
Sequence 69134, A
Sequence 69134, A
Sequence 6826, A
Sequence 6826, A
Sequence 6825, A
Sequence 55507, A
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2: /cgn2 6/ptodata/1/pubpaa/US08 PUBCOMB.pep:*
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(c) 1993 - 2005 Compugen Ltd.
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US-10-335-977-8629

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US-10-156-761-10253
US-10-424-599-254635
US-10-424-599-254635
US-10-428-21340
US-10-282-122A-6250
US-10-282-122A-62519
US-10-282-122A-64516
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US-10-282-122A-64616
US-10-282-122A-64616
US-10-282-122A-684616
US-10-282-122A-68482
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US-10-282-122A-56846
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100.0%; Pred. No. 3.4e-114;
iive 0; Mismatches 0;
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; Publication No. US20040005325A1
; GENERAL INFORMATION:
; APPLICATION RECEDENCE:
; TITLE OF INVENTION: Helicobacter vaccine
; FILE REFERENCE: Degoedesequenties
; CURRENT APPLICATION UNDER: US/09/904,994B
; CURRENT FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 21
                                                                                                                                                                                                                                                                                                                APPLICANT: AKZO NO. US20040005325A1e1 N.V.
TITLE OF INVENTION: Helicobacter vaccine
FILE REFERENCE: Degoedseequenties
CURRENT APPLICATION NUMBER: US/09/904,994B
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 226
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; Publication No. US20040005325A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Helicobacter felis
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Best Local Similarity 100.
Matches 226; Conservative
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US-09-904-994B-11
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                                                                                                                  Score 1178; DB 3; Length 226;
Pred. No. 7.1e-114;
1; Mismatches 0; Indels (
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Publication No. US20040005325A1
GENERAL INFORMATION:
TITLE OF INVENTION: Helicobacter vaccine
FILE REFERENCE: Degoedesequenties
CURRENT APPLICATION NUMBER: US/09/904,994B
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
                                                                                                                    Query Match
Best Local Similarity 99.6%;
Matches 225; Conservative
                                                                  ; ORGANISM: Helicobacter felis
US-09-904-994B-14
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SOFTWARE: Patentin Ver.
SEQ ID NO 14
LENGTH: 226
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Sequence 11, Application US/09904994B
Publication No. US20040005325A1
GENERAL INFORMATION:
APPLICANT: AKZO No. US20040005325A1e1 N.V.

RESULT 4 US-09-904-994B-11

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                                                                                                                                                                                                                                                                                           Score 1174; DB 3; Length 226;
Pred. No. 1.8e-113;
2; Mismatches 0; Indels (
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TITLE OF INVENTION: Helicobacter vaccine FILE REFREENCE: Degcedesequenties CURRENT APPLICATION NUMBER: US/09/904,994B CURRENT FILING DATE: 2001-07-13 NUMBER OF SEQ ID NOS: 21 SEGTWARE: Patentin Ver. 2.1 SEQ ID NO 11
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.1%;
Matches 224; Conservative
                                                                                                                                                                                                   TYPE: PRT ORGANISM: Helicobacter felis
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SEQ ID NO 8
LENGTH: 226
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Matches 223; Conservative
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61 GRTLLKADDVMPGVAHMIHEVGIEAGFPDGTKLVTIHTPVEAGSDKLAPGEVILK-NEDI 119
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                                                                                       ELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGA 179
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APPLICANT: Trawick, John D.
APPLICANT: Trawick, Grant J.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
APPLICANT: Yanamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITEA. 0.11A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 60/191,078
PRIOR FILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-05-26
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-10-23
PRIOR FILLING DATE: 2000-11-27
PRIOR FILLING DATE: 2000-12-26
PRIOR FILLING DATE: 2000-10-216
PRIOR FILLING DATE: 2000-10-216
NUMBER OF SEQ ID NOS: 14110
SEQ ID NO 11468
LENGTH: 238
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; Pred. No. 4.1e-55;
42; Mismatches 62;
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Best Local Similarity 53.1%;
Matches 119; Conservative 4:
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APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 ELNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 TLNAGKQATTLEVHNKGDRPVQVGSHFHFFEVNKLLEFDREKAYGKRLDIASGTAVRFEP 179
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                                                                APPLICANT: Chang, Yung-Fu
APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Shupson, Kenneth W
APPLICANT: Zhu, Jidajan
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: HE DIAGNOSTIC AND TREATMENT METHODS
FILE REFERENCE: 19603/881 US/10/639,273
CURRENT APPLICATION NUMBER: US/10/639,273
CURRENT FILING DATE: 2003-08-12
PRIOR APPLICATION NUMBER: 60/404,337
PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNOPEAIAYISAHIMDEARRGKKTVAQLMEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.2%; Score 652; DB 4; Length 234; 57.3%; Pred. No. 3.9e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 GQTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Helicobacter bizzozeronii
Sequence 3, Application US/10639273 Publication No. US20040142343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Helicobacter heilmannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 57.38
Matches 129; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-10-639-273-34
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SEQ ID NO 11286
LENGTH: 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                             APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
ELECTRIC ACID AND THEREAPEUTICS
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 238;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
S1.9%; Score 613.5; DB 4.
Best Local Similarity 53.1%; Pred. No. 4.1e-55;
Matches 119; Conservative 42; Mismatches 62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/335,977 FILING DATE: 30-Dec-2002 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...238

SEQUENCE DESCRIPTION: SEQ ID NO: 8629:

US-10-335-977-8629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GIN-018
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             NUMBER OF SEQUENCES: 10031
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKPIELD
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                             ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                 Sequence 8629, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 238 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 8629: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 02109-1875
                                                                                                                                                                                                                                                   CITY: Boston
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US-10-335-977-8629
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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Publication No. US20040142343A1

GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu

APPLICANT: Simpson, Kenneth W

TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES

TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS

FILE REFERENCE: 19603/3881

CURRENT APPLICATION NUMBER: US/10/639,273
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                                                                                                                 APPLICANT: Obligation, Kari L.
APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: 2yskind, Judith W.
APPLICANT: Trawick, John D.
APPLICANT: Trawick, John D.
APPLICANT: Yamamoco, Robert T.
APPLICANT: Yamamoco, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Dentification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
FILE REPERENCE: ELITRA.011A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2001.03.21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PLING DATE: 2000.03.21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000.05.23
PRIOR PILING DATE: 2000.05.26
PRIOR PLING DATE: 2000.05.26
PRIOR PLING DATE: 2000.05.26
PRIOR PLING DATE: 2000.10.23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PLING DATE: 2000.11.27
PRIOR PLING DATE: 2000.12.22
PRIOR PLING DATE: 2000.12.22
PRIOR PLING DATE: 2000.12.22
PRIOR PLING DATE: 2000.12.22
PRIOR PLING DATE: 2001.02.16
PRIOR PLING DATE: 2001.02.16
NUMBER OF SEQ ID NOS: 14110
Sequence 11286, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Helicobacter pylori
US-09-815-242-11286
                                                                 GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.7%
Matches 118; Conservative
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HYPOTHETICAL: YES ORIGINAL SOURCE:
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                                                            FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                    121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                 1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                 Gaps
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                            Query Match 50.3%; Score 594; DB 4; Length 237; Best Local Similarity 52.2%; Pred. No. 4.4e-53; Matches 117; Conservative 43; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROW ISO9660
COMPUTER: EDA FORM:
MEDIUM TYPE: CD/ROW ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
SOFTWARE: UNIX
CURRENT APPLICATION DATA:
FILING DATE: 30-Dec-2002
PRIOR APPLICATION NUMBER: US/10/335,977
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Mandragouras, Amy E. REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSE: LAHIVE & COCKFIELD
STREET: 28 State Street
PRIOR APPLICATION NUMBER: 60/404,337
PRIOR FILING DATE: 2003-08-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 36
LENGTH. 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8628, Application US/10335977
Publication No. US20040052799A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 8628:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 228 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                          TYPE: PRT
; ORGANISM: Helicobacter pylori
US-10-639-273-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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Helicobacter
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APPLICANT: Selig, Luc
TITLE OF INVENTION: Collection of Protein Interactions and Applications thereof
TITLE OF INVENTION: pylori Protein-Protein Interactions and Applications thereof
TITLE OF INVENTION: pylori Protein-Protein Interactions and Applications thereof
TITLE OF INVENTION: pylori Protein-Protein Interactions and Applications thereof
TITLE OF INVENTION: pylori Protein-Protein Interactions and Applications thereof
TITLE OF INVENTION NUMBER: US/10/012,819
TURRENT FILING DATE: 2001-10-30
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 154
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 DGVASMIHEVGIBAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDITINEGKKAVSVK 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 VTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAGQTRKVQLIPLG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72 PGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIELNAGKEVTELE 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 MLHYAGELAKKRKEKGIKLNYVEAVALISAHIMEEARAGKKTAAELMQEGRTLLKFDDVM
                                                                                                                                                                                                                                                                                                                  12 LLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEECMHFLKKDEVM
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                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                 DB 4;
                                                                                                                                                                                                 Query Match 48.8%; Score 576.5; DB 4 Best Local Similarity 52.6%; Pred. No. 2.7e-51; Matches 112; Conservative 40; Mismatches 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              192 GSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |:::: | | ||: || GRRIFGFNALVDRQADNESKKIALHRAKERGF 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41; Mismatches
                                                     NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...228
SEQUENCE DESCRIPTION: SEQ ID NO: 8628:
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 154, Application US/10012819
Publication No. US20030017478A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Helicobacter pylori
US-10-012-819-154
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Best Local Similarity
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                                                 Sequence 35, Application US/10639273
; Sequence 35, Application US/10639273
; Publication No. US20040142343A1
; Publication No. US20040142343A1
; GENERAL INFORMATION:
; APPLICANT: Chang, Yung-Fu
; APPLICANT: Zhu, Jiaqian
; TITLE OF INVENTION: HILLCOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
; TITLE OF INVENTION: LN DIAGNOSTIC AND TREATMENT METHODS
; FILE REFERENCE: 19603/381
; CURRENT APPLICATION WUMBER: US/10/639,273
; CURRENT FILING DATE: 2003-08-12
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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Publication No. US20040142343A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Show, Jiaqian
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
GURRENT APPLICATION NUMBER: US/10/639,273
CURRENT FILING DATE: 2003-08-12
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PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 41
SCOTHWARE: Patentin Ver. 2.1
LENGTH: 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Helicobacter felis
RESULT 14
US-10-639-273-35
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US-10-639-273-37
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                    61 GREILKADEVMEGVASMYNEVQVEVSFPDGTKLYTIHNPIEDNGKLTPGEYILK-DEDIT 119
                                                                                                                                                                         121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                   181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGFI 225
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RESULT 2
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50, Appl
1089, Ap
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244, App
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3184, Ap
2594, Ap
462, App
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Sequence 181, App
Sequence 2006, Ap
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1 WKLTPKEQEKFLLYYAGEVA.....ADERHKHKALDKAKSHGFIK 226
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/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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/cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-519-386-1086

US-10-689-742-50

US-10-821-234-1089

US-10-821-234-1089

US-10-793-626-1248

US-10-793-626-1248

US-10-793-626-1460

US-10-793-626-1460

US-11-013-759-3

US-11-013-759-7

US-11-013-759-7

US-11-013-759-7

US-11-013-759-7

US-11-013-759-7

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US-11-013-759-7

US-10-793-626-3188

US-10-793-626-3188
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 106, App
Sequence 272, App
Sequence 68, Appl
Sequence 962, App
Sequence 59, Appl
Sequence 17, Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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Publication No. US2055255478A1
GENERAL INFORMATION: US2055255478A1
GENERAL INFORMATION: STARHYLOCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STARHYLOCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TILE OF INVENTION: STARHYLOCCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 1999-11-09
PRIOR PILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 116
LENGTH: 111
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US-10-793-626-3250

US-10-793-626-2958

US-10-921-234-1262

US-10-921-934-1262

US-11-053-100-58

US-11-053-100-58

US-11-053-100-58

US-11-099-715-2

US-11-179-977-15-2

US-11-082-389-128

US-11-082-389-128

US-11-092-389-128

US-11-092-389-128

US-11-093-626-2174

US-10-793-626-2174

US-10-793-626-106

US-10-485-517-373

US-10-689-742-68

US-10-689-742-68

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Publication No. US20050256299A1
GENERAL INPORMATION:
APPLICANT: UNEXPERSITY of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Foster, Simon
TITLE OF INVENTION: Antigenic Polypeptides
TITLE REPERRING: P100629W0
CURRENT APPLICATION NUMBER: US/10/485,517
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ORGANISM: Artificial Sequence
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 ----VIVNWPIEPDEHFKAGEVKFGCDKDIELNAGKEVTELEVTNEGPKSLHVGSHFHFF 149
                                                                                                                                                                                                                                                                                                                                                                                                138 KSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAGOTRKVQLIPLGGSKKVI 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177 ----AKVKRIEKYGAFVELFPGKDALLHISQISQERINKVEDVIKIGDTIEVKITEIDK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                 MDEARRGK-----KTVAQLMEECMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKL-- 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2006, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
APPLICAT'S KINMERLY,
ITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFREENCE: PU3440US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PINOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 44772
SOFTWARE: PATENTIN VAI. 2.1
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                                                                                                                                                                                                                                                                                                                                                           Gaps
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US-10-793-626-2006
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                                                                                                                                                                                                                                                                                                       18.0%; Score 212; DB 1; Length 106; 46.9%; Pred. No. 2.4e-14; E. Mismatches 28; Indels
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0200349.9
PRIOR FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SOFTWARE: PATENTIN VETSION 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 NGLVNNIADERHKHKALDKAKS 221
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US-10-510-386-108
; Sequence 108, Application US/10510386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 GMNGLVNNIADERHKHKALDK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFRGMVNGPIDESRVYRPTDE 82
                                                                                                                                                                                                             ; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-485-517-181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                      38; Conservative
                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
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US-10-793-626-2006
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LENGTH: 247
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                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 FKAGEVKFGCDKDIELNAGKEVTELEVTNEGPKSLHVGSHF-----HFFEANKAL--- 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jacobs, Kenneth
APPLICANT: Jacobs, Menneth
APPLICANT: Lavallie, Edward R
APPLICANT: Lavallie, Edward R
APPLICANT: Racie, Lisa A
APPLICANT: Racie, Lisa A
APPLICANT: Racie, David
APPLICANT: Preacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REPERENCE: 00766.00091.0
CURRENT APPLICATION NUMBER: US/10/689,742
CURRENT FILING DATE: 2002-10-22
PRIOR FILING DATE: 2002-12-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LIPKEQEKFLLYYAGEVARKRAE--GLKLNQPEAIAYISAHIMDEARRGKKTVA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 RAVNFMGLLIENPKLDAKIFSAKGYGEPKPIASNDT-EEGRRKORRVEILILPIG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.6%; Score 77.5; DB 1; Length 259; Best Local Similarity 21.7%; Pred. No. 0.71; Matches 38; Conservative 36; Mismatches 54; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 428;
                                                                                APPLICANT: Clausen, ib Groth
APPLICANT: Olsen, reten Troels
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Ramussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REPERSHORS: 10294.204-US
CURRENT APPLICATION NUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SEQ ID NO 108
SEQ ID NO 108
LENGTH: 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 50, Application US/10689742
Publication No. US20050250180A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , ORGANISM: Bacillus licheniformis US-10-510-386-108
Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
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SEQ ID NO 50
LENGTH: 428
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US-10-689-742-50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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; Sequence 1248, Application US/10793626; Bublication No. US20050255478A1
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REPRENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT APPLICATION NUMBER: 06/164,258
; PRIOR FILINO DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SEQ ID NO 1248
; LENGTH: 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 H-----ELEVLSE---SLDLGQ------LIVERQRAKVSLVGKGLQAKVGLLTKM 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIGNINFSFITDDDGHSFHNFKKFTMP-IVQALQSMGVNAEMTGRNDIQVGQAKISGNAM 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      216 GAKVLHPDSVEYAQRFKVPLRVLSSFEAGOGTLIQFGDESELAMAASVOGIAINKALATL 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82 GVEATFPDGTKL------VTVNW--PIEPDE-----HFKAGEVKFGCDKDIEL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              122 NAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKA----YGKRLDIPSG---NT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GLKLNOPEAIAY----ISAHIMDEARRGKKTVAQLMEECMHFLKKDEVMPGVGNMVPDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHER INFORMATION: Description of Artificial Sequence: synthetic: OTHER INFORMATION: amino acid sequence US-10-793-626-1248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
6.0%; Score 71; DB 1; Length 311;
Best Local Similarity 18.9%; Pred. No. 3.9;
Matches 58; Conservative 35; Mismatches 100; Indels 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 LRIGAGOTRKVOLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
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APPLICANT: Yorgey, Peter S.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INVENTIONS TREATHER APPLICATION NUMBER: US/10/858,730
CURRENT APPLICATION NUMBER: US 60/475,000
PRIOR APPLICATION NUMBER: US 60/475,000
PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR APPLICATION NUMBER: US 60/551,860
PRIOR FILING DATE: 2003-05-30
PRIOR FILING DATE: 2004-03-10
NUMBER OF SEQ ID NOS: 364
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.1%; Score 72; DB 1;
Best Local Similarity 21.7%; Pred. No. 4.7;
Matches 50; Conservative 34; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Shewanella oneidensis US-10-858-730-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
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Publication No. US20050255114A1

GENERAL INFORMATION:

APPLICANT: Labar, Ivan

APPLICANT: Andarmani, Susan

APPLICANT: Andarmani, Susan

APPLICANT: Methods for Diagnosis and Treatment of Preeclampsia

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia

CURRENT APPLICATION NUMBER: US/10/821,234

CURRENT APPLICATION NUMBER: US 60/462,047

PRIOR PLING DATE: 2003-04-07

NUMBER OF SEQ ID NOS: 1704

SOFTWARE: Pt SEQ Genes Version 1.0

SEQ ID NO 1089
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       235 EIQVKPTCKPSWQGWNKRIEYAPGAGSL-----ALFP-GIRLETCDEPLWNIQATIEL 286
                                                          KAGEVKFGCDKD-----IELNAGKEVTELE-VTNEGPK-----SLHV---GSHFHFF 149
                                                                                                                                                               150 EANKALKFDREKAYGKRLDIPSGNTLRIGAGQTRKVQLIPLGGSKKVIGMNGLVNNIADE 209
                                                                                                                                                                                                                  ----VPLGGP-----SGLGSGPQDS 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 BINAGKEVTELEVTNEGPKSLHVGSHFH-----FFEANKALKFDR---EKAYGKRLDI 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VKLIPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CMHFLKKDEVMPGVGNMV-PDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6.2%; Score 73.5; Di
21.2%; Pred. No. 3.8;
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Doten, Reed
Driggers, Edward M.
Madden, Kevin T.
O'Leary, Jessica
O'Toole, George
Trueheart, Joshua
Walbridge, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/10858730 Publication No. US20050255568A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                    210 RHKHKALDKAKSHG 223
                                                                                                                                                                                                                                                                                                                       370 LSDHFTLSFWMKHG 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 21.2%
Marches 51, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1089
                                                                                                                                                                                                                  347 NGTQAVQ---
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
US-10-821-234-1089
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Length 418; 82; Indels

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US-10-793-626-244
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US-10-793-626-244
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LENGTH: 501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 WPIEPDEHF---KAGEVKFGCD----KDIELNAGKEVTE-LEVTNEGPKSLHVGSHFHFF 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 LKLKELEHLINNNKLHEYLASFÖKESAKDÍHPNNRKRVLRAIÉYYLKTKKLLSSRKKVOOF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EANK-----ALKFDREKAY---GKRLDIPSGNTLRIGAGQTRKVQ-LIPLG----GSKKV 196
                      176 IDIEEFKKIILKTIFGENEVEEYILTEEDWKNIKQLSDEKYRTWEWNYGSNPKYNIEREE 235
                                                                                                                                          162 AYGK----RLDIPSGNTLR-----IGAGQTRKVQLIPLGGSKKVIGMNGLVNNIADE 209
                                                                                                                                                                ------EVTELEVINEGPKSLHVGSHFHP-----FEANKALKFDREK 161
                                                                                                                                                                                                                                                                                                                             Sequence 1460, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
TITLE PEPERENCE: PU3480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT PILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1460
LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 HIMDEARRGKKTVAQLMEECMHFLKKDEVMPGVGNMVPDLGVEATFPDGT----KLVTVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: synthetic; OTHER INFORMATION: amino acid sequence US-10-793-626-1460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
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 VTVNWPIEPDEHFKAGEVKFGCD-----KDIELNAGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Conservative
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Best Local Similarity
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99 VSFADSDIVPPASTWVFPTLGIMHHNKQATENAKEEVRRILGLLDAYLKTRTFLVGERVT 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 244, Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REPRENCE: PUBLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT FILING DATE: 2004-03-04
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                       82; Gaps
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                                                                                                                                                                                                                                                                                                                               DB 1; Length 437;
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12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 AGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKR 166
                                                                                                                                                                                                                                                                                                                                                                                    Indels
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5.8%; Score 69; July
Best Local Similarity 20.0%; Pred. No. 12;
Matches 42; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                               5.9%; Score 70; DB 1
20.5%; Pred. No. 7.8;
iive 31; Mismatches
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CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PLILIGATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: DE SEQ_Genes Version 1.0
SEQ ID NO 1668
LENGTH: 437
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Best Local Similarity 20.59
Matches 46; Conservative
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162 AYGKRLDIPSGNTLRI-
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; Publication No. US20050249747A1
; GENERAL INFORMATION:
    APPLICANT: Loosmore, Sheena M.
    APPLICANT: Sasaki, Ken
    APPLICANT: Sasaki, Ken
    APPLICANT: Klein, Michel H.
    TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
    TITLE OF INVENTION: PROTEIN OF MORAXELLA
    TITLE OF INVENTION: PROTEIN OF MORAXELLA
    FILE REFERENCE: 1038-921MIS:jb
    CURRENT APPLICATION NUMBER: US/19/361,619
    FRIOR APPLICATION NUMBER: US/09/361,619
    FRIOR PLING DATE: 1999-07-27
    NUMBER OF SEQ ID NOS: 32
    SOFTWARE PATENTIN Ver. 2.1
    SEQ ID NO 13
    LENGTH: 1992
    TYPE: RPT
    ORGANISM: MOTAXELIA CREATRABIS
    ORGANISM: MOTAXELIA CREATRABIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 KAGEVKFGCDKDIELNAGKEVTE----LEVTNEGPKSLHVGSHFHFFFANKALKFDREK 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 AYGKRLDIPSGNTLRI-----GAGQTRK------VQLIPLG---GSKK 195
                                                                                                                                                                                                                            APPLICANT: Sasaki, Ken
APPLICANT: Yang, Yan Ping
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REFERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT APPLICATION NUMBER: US/09/361,619
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 3.3
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25.0%; Pred. No. 92;
tive 18; Mismatches 47; Indels 49
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5.8%; Score 68.5; DB 7; Length 1992;
Best Local Similarity 25.0%; Pred. No. 92;
Matches 38; Conservative 18; Mismatches 47; Indels 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Moraxella catarrhalis
US-11-013-759-3
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Best Local Similarity 25.0%
Matches 38; Conservative
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SUBJECTANT: LOCSHOLIAN:
APPLICANT: ASBARI, Ken
APPLICANT: SASARI, Ken
APPLICANT: Yang, Yan Fing
APPLICANT: Yang, Yan Fing
APPLICANT: Yang, Yan Fing
APPLICANT: Yang, Wan Pang
APPLICANT: Yang, Yan Fing
APPLICANT: Yang, Wanchel H.
TITLE OF INVENTION: PROTEIN OF MORAXELLA
CURRENT APPLICATION NUMBER: US/11/013, 759
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR PILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PALENTING DATE: 2.1
SEQ ID NO 4
LENGTH: 2047
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APPLICANT: LOOSEMORE, Ken
APPLICANT: Sasaki, Ken
APPLICANT: Yang, Yan Ping
TITLE OF INVENTION: PECOMPINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
TITLE OF INVENTION: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/09/361,619
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATCHLIN Ver. 2.1
SEQ ID NO 7
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                                     ---- VQLIPLG---GSKK 195
                                                                                                                                                                              675 VNGSNPGTGIANTARITRDKIGFAGSDGAVDTNKPYLDQDKLQVGNVKITNTGINAGGKA 734
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5.8%; Score 68.5; DE
Best Local Similarity 25.0%; Pred. No. 96;
Matches 38; Conservative 18; Mismatches
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Publication No. US20050249747A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Moraxella catarrhalis
US-11-013-759-4
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US-09-338-920B-11
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Sequence 2, Appli
Sequence 5, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 22, Appli
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                                                                                                                    November 28, 2005, 08:13:38; Search time 18.5013 Seconds (without alignments) 1009.915 Million cell updates/sec
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1 VKLTPKEQEKFLLYYAGEVA.....ADERHKHKALDKAKSHGFIK
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
5.1.6
Compugen Ltd.
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5-09-489-039A-9261
5-07-732-242C-1
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5-09-134-001C-5049
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US-08-920-095-2
US-08-920-095-2
US-09-338-920B-5
US-09-331-705-4
US-08-467-822-22
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US-08-467-822-20
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US-08-466-248-25
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
GenCore (c) 1993
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Maximum DB seq length: 2000000000
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No.
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61 GRTLLKADDVMPGVAHMIHEVGIEAGFPDGTKLVTIHTPVEAGSDKLAPGEVILK-NEDI 119
                      18, Appl
26884, A
116, App
6085, Ap
                                                                        2, Appli
59, Ap
10, Appli
4, Appli
926, Ap
24, Appli
24, Appl
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Sequence 926
Sequence 24,
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GENERAL INFORMATION:
TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE
TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 234;
                                                                                                                                                                                                                                                                                                           Sequence 11, Application US/09338920B
Fatent No. 6709851
GENERAL INFORMATION:
APPLICANT: Soman, Gopalan
FILE APPLICANT: Thomas, William D., Jr.
APPLICANT: Monath, Thomas P.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 60132/023002
CURRENT FILING DATE: 2002-12-23
FRIOR APPLICATION NUMBER: US 08/928,081
FRIOR APPLICATION NUMBER: US 08/928,081
FRIOR PILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 234
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                      US-09-602-777A-18
US-09-522-91A-26884
US-09-710-279-116
US-09-713-681A-6085
US-07-732-242C-2
US-09-328-325-5915
US-09-602-77A-10
US-08-607-77A-10
US-08-687-645B-4
US-08-489-039A-9266
US-08-487-645B-4
US-08-487-645-24
US-08-466-248-24
US-08-456-248-24
US-08-456-248-24
US-08-456-248-24
US-09-134-001C-4415
US-09-134-001C-4415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.7%; Score 622; DB 2; Best Local Similarity 54.7%; Pred. No. 2.9e-62; Matches 123; Conservative 41; Mismatches 59.
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TYPE: PRT
ORGANISM: Helicobacter pylori
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                                                          US-09-338-920B-5
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PCT-US96-05800-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09338920B
Patent No. 6709581
GENERAL INFORMATION:
APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas P.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 06132/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR APPLICATION NUMBER: US 08/928,081
NUMBER OF SEQ ID NOS: 14
SOTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62; Indels
                                                                                                                                                                                COMPUTER: . IBM PC compatible
OPERATING SYSTEM: PC.DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,095
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/431,041
FILING DATE: 28-APR-1995
ATTONEXYAGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          06132/013001
                                     E: Fish & Richardson P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REPERENCE/DOCKET NUMBER: 061
TELECOMMUNICATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (617) 542-8906
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                           ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 238 amino acids
amino acid
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Matches 118; Conservative
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NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                            Boston
                                                                                                                 USA
                                       ADDRESSEE:
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US-09-338-920B-5
                                                                                                               COUNTRY:
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                    Gaps
                                                    1;
Length 238;
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GENERAL INFORMATION:
APPLICANT: OraVax, Inc.
TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                            181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PPLICATION NUMBER: PCT/US96/05800 FILING DATE: 23.APR-1996 CLASSIFICATION:
DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4
  Query Match 51.7%; Score 610.5; DB Best Local Similarity 52.7%; Pred. No. 6.1e-61 Matches 118; Conservative 43; Mismatches 6
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APPLICATION NUMBER: 08/431,041
FILING DATE: 28-APR-1995
CLASSIPICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,122
FILING DATE: 06-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T:
REFERENCE/DOCKET NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/0;
TELECOMMINICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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FORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
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FILING DATE:
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                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/09431705
Sequence 4, Application US/09431705
Patent No. 6585975
GENERAL INFORMATION:
APPLICANT: Londono-Arcila, Patricia
APPLICANT: Ereeman, Donna
TITLE OF INVENTION: Use of salmonella vectors for
TITLE OF INVENTION: Use of salmonella vectors for
TITLE OF INVENTION: Use of salmonella vectors for
CURRENT APPLICATION VUMBER: US/09/431,705
CURRENT APPLICATION NUMBER: US/09/431,705
CURRENT FILING DATE: 1999-11-01
SOURMARE: PastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
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                  62; Indels
52.7%; Pred. No. 6.1e-61;
ive 43; Mismatches 62
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Patent No. 6709851
GENERAL INFORMATION.
APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Monath, Thomas P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
 Best Local Similarity 52.7%
Matches 118; Conservative
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US-09-338-920B-7
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US-09-431-705-4
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GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Labigne, Aches
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: HMUNOGRNIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
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                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
TITLE OF INVENTION: Stabilization of Helicobacter Urease FILE REFERENCE: 06132/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR APPLICATION NUMBER: US 08/928,081
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
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MEDLUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ELOPPy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                    51.1%; Score 603.5; DB 2
52.2%; Pred. No. 3.8e-60;
tive 43; Mismatches 63
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APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
FLIASSIFICATION: APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JMBER: US 08/432,697
02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 22, Application US/08467822
; Patent No. 5843460
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                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-338-9208-7
                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 52.2
Matches 117; Conservative
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TELECOMMUNICATION INFORMATION
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Sequence 22, Application US/08432697

Patent No. 6246330

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Farero, Richard L.

APPLICANT: Farero, Richard L.

APPLICANT: Frerero, Richard L.

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST

TITLE OF INVENTION: POLYPEPTIDES FOR USE IN THE

TITLE OF INVENTION: POLYPEPTIDES

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCES: Hunegan, Henderson, Farabow, Garrett & STREED CORRESEES: Punneral Control of Control of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50.8%; Score 600; DB 1; Length 237; 52.7%; Pred. No. 9.4e-60; Live 43; Mismatches 61; Indels
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COUNTRY: USA
ZIP: 20005-3315
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FTING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCEY/COCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
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REFERENCE/DOCKET NUMBER: 03495.0137-00000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 52.73
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 GRILLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTFIEANGKLVPGEL-FLKNEDIT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
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                                                                                                                                                                                                                                                                                                                                                                                                1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                             Gaps
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7
                                                                                                                                                                                                                                                                                    50.8%; Score 600; DB 2; Length 237; 52.7%; Pred. No. 9.4e-60; ive 43; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURPOLER: THE F. COMPACLING SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRICE 19-MAY-1995
FILING DATE: 19-MAY-1995
CLASSIFICATION NUMBER: US 08/417,177
FILING DATE: 19-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: US-MAY-1995
CLASSIFICATION NUMBER: US 08/432,697
FILING DATE: US-MAY-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
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IBM PC compatible
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TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 22
SEQUENCE CHARACTERISTICS:
                                                                                                   LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPCLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.7%
Matches 118; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PO
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APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
    121 VKAVGDRPVQIGSHFHFFEVNRCLDFDREKTFGKRLDIASGTAVRFEPGEEKSVELIDIG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MKLTPKELDKLMLHYAGRLAEERLARGVKLNYTEAVALISGRVMEKARDGNKSVADLMQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.5%; Score 572.5; DB 1; Length 237; 50.4%; Pred. No. 1.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1..237
OTHER INFORMATION: /note= "URE A - FIGURE 3."
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                                                                              192 GSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADPLICATION NUMBER: US 08/467,822
FILING DATE: 06-JUN-1995
CLASSIPTCATION: 435
FLOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIPTCATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIPTCATION ATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIPTCATION NUMBER: US 08/432,697
FILING DATE: XENILET NUMBER: 25,146
RECERENCE/DOCKET NUMBER: 25,146
REPERENCE/DOCKET NUMBER: 25,146
REPERENCE/DOCKET NUMBER: 25,146
                                                                                                                                                                                                               Sequence 20, Application US/08467822 Patent No. 5843460 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3315
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                                                                                                 셤
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Patent No. 6916615

GENERAL INFORMATION:
APPLICANT: Legrain, Pierre
APPLICANT: Selig, Luc
APPLICANT: Rain, Jean-Christophe
TITLE OF INVENTION: Collection of Prokaryotic DNA for Two-Hybrid System, Helicobacter
FITLE OF INVENTION: pylori Protein-Protein Interactions and Applications thereof
FILE REFERENCE: B5053
CURRENT APPLICATION NUMBER: US/10/012,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 DGVASMIHEVGIEAMPPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDITINEGKKAVSVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 GRTLLKPDDVMDGVASMIHEVGIEAMFPDGTKLVTVHTPIEANGKLVPGEL-FLKNEDIT 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 PGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIELNAGKEVTELE 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 VTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAGGTRKVQLIPLG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 LLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEECMHFLKKDEVM 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                    Length 237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 EEKSVELIDIGGNRRIFGFNALVDRQADNESKKIALHRAKERGF 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                                                                 50.8%; Score 600; DB 2;
52.7%; Pred. No. 9.4e-60;
iive 43; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .2e-57
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.1%; Pred. ....
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PRIOR APPLICATION NUMBER: EP 99401066.8
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 278
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 52.79
Matches 118, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 111; Conservative
                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                         linear
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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
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                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Thiberge, Michard L.
TITLE OF INVENTION: IMMUNCENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: OMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
                                                                                                                                   CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                             LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
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                                                                                                                                                                                                                       181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SISTEM: r-LUCS, ms-LUCS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-00000
TELEPHONE: (202) 408-4400
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Protein
LOCATION: 1..237
OTHER INFORMATION: /note= "URE A - FIGURE 3."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 Sequence 20, Application US/08432697 Patent No. 6248330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 237 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 50.4<sup>§</sup>
Matches 113<sup>;</sup> Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
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US-08-432-697-20
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Sequence 20, Application US/08466248
Patent No. 6258359
GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                             Length 237;
                                                                                                                                                                                                180 EEKSVELIDIGGNKRIYGFNSLVDROADADGKKLGLKRAKEKGF 223
                                                                                                                                                                      181 OTRKVOLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/466,248 FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 I Street, N.W. CITY: Washington STATE: D.C.
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..237
; COTHER INFORMATION:
US-08-466-248-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Protein
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48.5%; Score 572.5;

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61 CMHFLKKDEVMPGVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIE 120
                                                                                                                                                                                               121 LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                   LNAGKEVTELEVTNEGPKSLHVGSHFHFFEANKALKFDREKAYGKRLDIPSGNTLRIGAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 INAGKEAISLKVKNKGDRPVQVGSHFHFFEVNKLLDFDRAKSFCKRLDIASGTAVRFEPG 179
                                                                        1 VKLIPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
                                                  1 VKLTPKEQEKFLLYYAGEVARKRKAEGLKLNQPEAIAYISAHIMDEARRGKKTVAQLMEE
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                  Gaps
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                                                                                                                                                                                                                                                                                          181 QTRKVQLIPLGGSKKVIGMNGLVNNIADERHKHKALDKAKSHGF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68; Indels
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                67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 06132/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR FILING DATE: 1997-09-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/09338920B
Patent No. 6709851
GENERAL INFORMATION:
APPLICANT: Soman, Gopalan
APPLICANT: Thomas, William D., Jr.
APPLICANT: Monath, Thomas P.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 06132/023002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 48.0%; Score 566.5; DB 2
Best Local Similarity 50.0%; Pred. No. 6.1e-56;
Matches 112; Conservative 43; Mismatches 68
; Pred. No. 1.3e-56; 43; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application US/09138920B
Patent No. 6709851
50.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Helicobacter felis
                Matches 113; Conservative
Best Local Similarity
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US-09-338-920B-9
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GVGNMVPDLGVEATFPDGTKLVTVNWPIEPDEHFKAGEVKFGCDKDIELNAGKEVTELEV 132
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                                                                                                                                                                                                                                                                                                           13 LYYAGEVARKRKAEGLKINQPEAIAYISAHIMDEARRGKKTVAQIMEECMHFLKKDEVMP
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                  Length 213;
                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                  Query Match 46.1%; Score 544.5; DB 2; Best Local Similarity 52.3%; Pred. No. 1.6e-53; Matches 112; Conservative 36; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SKKVIGMNGLVNNIADERHKHKALDKAKSHGFIK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 NORIFGFNDLNNGOVNEDNKRKALAAAKAKGFIK 213
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PASLES for Windows Version 4.0
SEQ ID NO 13
LENGTH: 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: November 28, 2005, 08:25:40 Job time : 19.5013 secs
                                                                                                                                                TYPE: PRT
ORGANISM: Helicobacter mustelae
                                                                                                                                                                                   US-09-338-920B-13
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

November 28, 2005, 08:00:02; Search time 36.4836 Seconds (without alignments) 1497.963 Million cell updates/sec

US-09-904-994B-3
2999
1 MKMKKQEYVNTYGPTKGDKV......KLCTSKPTSQVPLAQRYTFF 568 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:\*
1: pirl:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	urease (EC 3.5.1.5	ä	urease (EC 3.5.1.5	urease alpha subun	dus sub	urease (EC 3.5.1.5	urease alpha chain	urease (EC 3.5.1.5	urease alpha subun	ang	.1.	urease (EC 3.5.1.5	.5.1.	3.5.1.	urease (EC 3.5.1.5	probable urease st	alpha sub	probable urease F1	alpha			ьa	5.1.	3.5.1.	ij	urease (EC 3.5.1.5	3.5.1.	urease (EC 3.5.1.5	urease complex com
	ΙD	URKCBP	835291	C36950	F83681	D69729	875169	AG2264	S47104	H83037	C75586	H64075	C36138	S42607	D43719	508480	G85654	D90794	A96699	A97648	AG2871	AF3458	E90027	S38485	$\sim$	URJB	AI3332	T37939	836028	G82890
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* Query	Match		74.8	٠			4.	63.3	63.0	61.1	•			•	60.5	。			ö	•	٥,	φ.	ď	•	٥.	æ.	7.	57.0		56.6
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Result	No.	1	7	٣	4	Ŋ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable ureC prot	urease (EC 3.5.1.5	collapsin response	dihydropyrimidinas	dihydropyrimidinas	dihydropyrimidinas	hypothetical prote	Ulip protein - mou	dihydroorotase (EC	allantoinase BH230	aminoacylase (EC 3	dihydropyrimidinas				
B70665	S10032	T29056	T50711	T08993	S42592	S58889	JC5317	S49985	JC5316	A83673	S55525	AC3412	E83938	JC4394	JC5318
		٠.	~	~	~	0	N	N	N	~	a	N	~	~	~
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577 2	614 1	558	569	129	131	572	572	572	572	448	570	478	438	484	570
	50.2 614 1												5.4 438		
53.7		40.9	38.2	14.4	10.6	6.2	5.8	5.8	5.7	5.5	5.4	5.4		5.3	5.3

## ALIGNMENTS

 RESULT 1 URKCBP urease (EC 3.5.1.5) 62K chain - Helicobacter pylori (strains 26695, J99, and others) N;Alternate names: urease beta chain; urease chain B; urease large subunit
 C;Species: Helicobacter pylori C;Date: 30-Sep-1991 #sequence revision 02-Dec-1994 #text_change 05-Oct-2004 C;Accession: B38537; H64288; A11977; F41834; S07885; S12487; A49215; B61371; A35306; B41 R;Labigne, A.; Cussac, V.; Courcoux, P.
 <ol> <li>Bacteriol. 173, 1920-1931, 1991</li> <li>A;Title: Shuttle cloning and nucleotide sequences of Helicobacter pylori genes responsib A;Reference number: A38537; MUID:91161505; PMID:2001995 A:Accession: B38537</li> </ol>
 A; Molecule type: DNA A; Residues: 1-569 < LAB> A; Residues: 1-569 < L
 Kiromb, J.F.; Mnite, U.; Astravage, A.K.; Claytou, K.A.; Surcon, G.G.; Freschmann, K.D.; Speterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenne son, J.D.; Kalley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Nature 188 639-547 1997
 A.Authors: Wallin, B.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A,Title: The complete genome sequence of the gastric pathogen Helicobacter pylori. A;Reference number: A64520; MUID:97394467; PMID:9252185
 A;Accession: notage A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A;CESIGUES: 1-599 A.LOM; A;CROSS-references: UNIPARC:UPI000002C20A; GB:AE000529; GB:AE000511; NID:g2313152; PIDN: A;Experimental source: strain 26695 B;Alm, R.A.; Ling, L.S.L.; Molr. D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; F;Alm, R.A.; Ling, D.S.L.; Molr. D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; F.Veor C. Gibeon B. Marberd D. Wills, S. D.; Jiang, O.; Tavlor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999 A,Title: Genomic sequence comparison of two unrelated isolates of the human gastric path A,Feference number: A71800; MUID:99120557; PMID:9923682
 A;Molecule type: DNA A;Residues: 1-569 <arn> A;Cross-references: UNIPARC:UPI000002C20A; GB:AE001446; GB:AE001439; NID:g4154573; PIDN: A;Experimental source: strain J99</arn>
 K;Uussac, V.; Ferrero, K.L.; Ladolgne, A.  J. Bacteriol. 174, 2466-2473, 199 A;Title: Expression of Helicobacter pylori urease genes in Escherichia coli grown under A;Reference number: A41834; MUID:92210488; PMID:1313413 A;Accession: F41834
 A.Status: preliminary A.Molecule type: DNA A.Residues: 565-569 <cus> A.Residues: 565-569 <cus> A.Cross-references: UNIPARC:UPI000002D2AD; GB:M84338 A.Cross-references: UNIPARC:UPI000002D2AD; GB:M84338 R.Clayton, C.L.; Pallen, M.J.; Kleanthous, H.; Wren, B.W.; Tabaqchali, S. R.Clayton, C.L.; 362, 1990 A.Title: Nucleotide sequence of two genes from Helicobacter pylori encoding for urease s A.Reference number: S07884; MUID:90221820; PMID:2326167 A.Accession: S07885</cus></cus>

302

301

421 422 481 482 541 542

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A;Accession: S35291
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-569 <FER>
A;Cross-references: UNIPROT:Q08716; UNIPARC:UPI000002F34B; EMBL:X69080; NID:G396160; PIDI
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CjComplex: heterodimer
CjFunction: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and tw
AjBescription: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and tw
CjFunction: heterodimer; hydrolase; metalloprotein; nickel
CjFunction: heterodimer; hydrolase; metalloprotein; nickel
Fj1-559/Product: urease 62K chain #status experimental <MAT>
Fj1-559/Product: urease 62K chain homology <UG2>
Fj1-351/Domain: urease 62K chain homology <UG2>
Fj1-351/Jeflomain: urease 62K chain homology <UG2>
Fj1-351/Jeflomain: urease 62K chain homology <UG3>
Fj1-351/Jeflomain: urease 62K chain homology (UG3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      303 TIPPTVNTEAEHMDMLMVCHHLDKSIKEDVQFADSRIRPQTIAAEDTLHDMGIFSITSSD 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKMNLHRM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N'Alternate names: urease beta chain
C;Species: Helicobacter felis
C;Date: 31-Dec-1993 #sequence_revision 02-Dec-1994 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 KISRKEYVSMYGPITGDRVRLGDIDLILEVEHDCTITYGEEIKFGGGKTIRDGMSQINSPS
                                                                                                                                                                                                                                                                                                                               243 VQVAIHTDTLNEAGCVEDTMAAIAGRIMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 SQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  482 GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 483 GKAKYDANITFVSQAAYDKGIKEELGLERQVLPVKOCRNITKKDMQFNDTTAHIEVNPET
                                                                                                                                                                                                                                                                                                                                                                                                                                            302 TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362 SQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        422 IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: S35291 K.f., Labigne, A. R:Ferrero, R.L.; Labigne, A. Mol. Microbiol. 9, 322-313, 1993 A;Title: Cloning, expression and sequencing of Helicobacter felis urease A;Reference number: S35290; MUID:94018627; PMID:8412683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        urease (EC 3.5.1.5) 62K chain - Helicobacter felis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : |||||| :: || :: |
543 YHVFVDGKEVTSKPANKVSLAQLFSIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 72.5% Matches 411; Conservative
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A.Residues: 1-9, A'.II-103, 'T',105-180,'F',182-192,'F',194-217,'L',219-272,'Y',274-539,'
A.Rosidues: 1-9, A'.II-103,'T',105-180,'F',182-192,'F',194-217,'L',219-272,'Y',274-539,'
A.Cross-references: UNIPARC: UPTO00002DB19; EMBL:X17079; NID:943633; PIDN:CAA34933.1; PII
R.Turbett, G.R.: Hoj, P.B.: Horne, R.; Mee, B.J.
Infect. Infect. of R.: Hoj, P.B.: Horne, R.; Mee, B.J.
Infect. Infect. of R.: Hoj, P.B.: Horne, R.; Mee, B.J.
A.Fille: Purification and characterization of the urease enzymes of Helicobacter species
A.Focession: A42215
A.Status: Preliminary
A.Molecule Fype: procein
A.Residues: J-12 -70Rs
A.Residues: J-12 -70Rs
A.Residues: J-12 -70Rs
A.Ross-references: UNIPARC:UPI0000BB645; PIDN:AAB24355.1; PID:9260964
A.Residues: J-12 -70Rs
A.Note: sequence extracted from NCBI backbone (NCBIP:119482)
R.Forsas verences: UNIPARC:UPI0000BB645; PIDN:AAB24355.1; PID:9260964
A.Note: sequence extracted from NCBI backbone (NCBIP:119482)
R.Forsas verences: UNIPARC:UPI0000DB645; PIDN:AAB24355.1; PID:9260964
A.Note: sequence extracted from NCBI backbone (NCBIP:119482)
R.Forsas verences: UNIPARC:UPI0000DB645; PIDN:AB24355.1; PID:9260964
A.Note: sequence extracted from NCBI backbone (NCBIP:119482)
R.Forsas verences: UNIPARC:UPI00000172DA7
A.Accession: B61371; MUID:91312104; PMID:1857197
A.Accession: B61371
A.Forsas-references: UNIPARC:UPI00000172DA7
A.Forsas-references: UNIPARC:UPI0000083DE0
A.Fille: Purification and characterization of urease from Helicobacter pylori.
A.Forsas verences: UNIPARC:UPI0000083DE0
A.Fille: Purification and characterization of urease from Helicobacter pylori.
A.Forsas verences: UNIPARC:UPI0000083DE0
A.Fille: David A.Forsas verences: UNIPARC:UPI0000083DE0
A.Fille: David A.Forsas verences: UNIPARC:UPI000083DE0
A.Fille: David A.Forsas verences: UNIPARC:UPI0000083DE0
A.Fille: David A.Forsas verences: UNIPARC:UPI0000083DE0

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A; Reference number: A41502; MUD: 90202165; PMID: 2318539
A; Accession: B41502
A; Molecule type: protein
A; Residues: 1-5, 'A', 7-15 < HUA>
A; Cross-references: UNIPARC: UP10000172DA8
C; Genetics:
A; Gene: ureB; HP0072
C; Complex: heterodimer of 26K chain (see PIR: URKCAP) and 62K chain
C; Function:
A; Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and tw
C; Superfamily: urease, alpha subunit; urease 62K chain homology
C; Superfamily: urease, alpha subunit; urease 62K chain homology
C; Superfamily: urease 62K chain homology (52,2)
C; Superfamily: urease 62K chain homology (62,2)
F; 136, 138, 219, 36Z Binding site: nickel 2 (His, His, Lys, Asp) #status predicted
F; 219, 248, 274/Binding site: nickel 1 (Lys, His) His) #status predicted
F; 219/Binding site: carbon dioxide (Lys) (covalent) (by urease activase) #status predict
F; 221, 322/Active site: His #status predicted
A;Molecule type: DNA
A;Residues: 1-9,'A',11-18,'A',20-103,'T',105-180,'F',182-192,'F',194-217,'L',219-272,'Y'
A;Cloys-references: UNIPARC:UF10000172DA6; EMBL:X17079
R;Clayvon, C.L.
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                                                                                                                                                                                                                              submitted to the EMBL Data Library, October 1989
A;Reference number: $12487
A;Accession: $12487
A;Molecule type: DNA
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A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-571 <5T7>
A;Residues: 1-571 <5T7>
A;Cross-references: UNIPARC:UPI00000C3801; GB:AP001507; GB:BA000004; NID:g10172612; PIDN
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                 urease alpha subunit ureC [imported] - Bacillus halodurans (strain C-125)
C,Species: Bacillus halodurans
C,Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
                                                                                                                        RMDVQVAIHTDTLNEAGFVEDTIKAIGDRVIHTYHTEGAGGGHAPDIMKVAGLPNVLPSS
VQVAIHTDTLNEGGFVEDTLKAIDGRVIHTYHTEGAGGGHAPDIIKAAGFPNILPSSTNP
                                                                                                    SQAMGRAGEVI PRIWOTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                                                                                        GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
                                                                                                                                                                                                                                                                  59 SPDENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 ALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 HRMLRAABEYSMNVGFLGKGNSSSKKQLVBQVEAGAIGFKLHEDWGTTPSAIDHCLSVAD
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C;Superfamily: urease, alpha subunit; urease 62K chain homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67.2%; Score 2016.5; DB 2; 64.4%; Pred. No. 1.6e-136; iive 88; Mismatches 112;
                                                                                                                                                                                                                                                                                                                542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                  :|| ||||| | :| | :||||| | 543 YEVKVDGQLVTCEPAEIVPMAQRYFLF 569
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Matches 368; Conservative
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C36950
urease (EC 3.5.1.5) 61k chain - Bacillus sp. (strain TB-90)
NyAlternate names: ureC protein
C;Species: Bacillus sp.
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 05-Oct-2004
C;Accession: C36950
R;Maeda, M.; Hidaka, M.; Nakamura, A.; Masaki, H.; Uozumi, T.
J; Bacteriol: 176, 432-442, 1994
A;Title: Cloning, sequencing, and expression of thermophilic Bacillus sp. strain TB-90 u
A;Reference number: A36950; MUID:94117379; PMID:8288539
A;Accession: C36950
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-569 «MAE>
A;Cross-references: UNIPROT:Q07397; UNIPARC:UPI0000137D67; GB:D14439; NID:g393296; PIDN:
C;Superfamily: urease, alpha subunit; urease 62K chain homology
C;Keywords: hydrolase
F;5-552/Domain: urease 62K chain homology <
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                                                      243 VQVAIHTDTLNEAGCVEDTLEAIAGRTIHTFHTEGAGGGHAPDVIKMAGEFNILPASTNP 302
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     AEGLIVTAGGIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRANLKSM 182
                                                                                                        VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP 301
                                                                                                                                                                           TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD 361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
N;Alternate names: protein s111750
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S75169
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-116, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross_references: UNIPROT:P73061; UNIPARC:UP10000137D79; EMBL:D90903; GB:AB001339; NID A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996 C;Genetics:
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                                                                            SSDSQAMGRAGEVIPRTWQTADKNKKEFGKLP-EDGKDNDNFRIKRYISKYTINPALTHG
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A,Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Accession: D69729
R;Kunst, F: Ogaawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J.; Pabret, C.; Ferrari, B.
Natthors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Galizzi, A.; Galler
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funa, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstehn, G.; Krogh, S.; Kunano, M.; Kurter, K.; Lapidus, A.; Ladalloris, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauch
R;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Parro, V.; Pohl, T.M.; Portetelle
R;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Sarahon,
R;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Sarahon,
R;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Sarahon,
R;Authors: Yoshikawa, H.F.; Zumatein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The Complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033; PMID:9384377
A;Residues: 1-569 <KUN>
A;Residues: 1-569 <KUN-
B;Residues: 1-560 <KUN-
B;Residues: 1-560 <K
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                                                                            119 ALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNL 178
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  SSDSQAMGRVGEVIIRTWQTADKMKKQRGALAEDQGKGNDNVRIKRYVSKYTINPAITHG 420
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                                                    VSEYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREM
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C;Superfamily: urease, alpha subunit; urease 62K chain homology
F;3-552/Domain: urease 62K chain homology <U62>
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                                                                                                                                                                                                                                                         DPKTFEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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A;Residues: 1-569 <MOE>
A;Cross-references: UNIPROT:P41020; UNIPARC:UPI0000137D66; EMBL:X78411; NID:g498708;
C;Genetics:
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#text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||: :|:| :||| ||: ||| ||:||| ||| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 SPDENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMODGVSPHMVVGVGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 ALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 HRMLRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVAD
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                                                                                                                                                                                                                                                                                                                                                                                         urease (EC 3.5.1.5) 62K chain - Bacillus pasteurii
N;Alternate names: ureC protein
C;Species: Bacillus pasteurii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-;
C;Accession: 847104
R;Moersdorf, G.; Weinmann, P.; Kaltwasser, H.
R;Moersdorf, G.; Weinmann, P.; Kaltwasser, H.
R;Moerstorf, G.;Morleotide sequence of three genes on a urease encoding I
A;Reference number: 847102
A;Accession: S47104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Gene: ureC
A,Start codon: GTG
C,Superfamily: urease, alpha subunit; urease 62K chain homology
C,Keywords: heterodecamer; hydrolase; metalloprotein; nickel
F;3-552/Domain: urease 62K chain homology <UG2>
F;3-552/Domain: urease 62K chain homology (U62>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 569;
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Matches 337; Conservative 112; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.0%; Score 1889.5;
                                                                                                                                                                                                                                        541 SYEVRADGELLTCEPATVLPMAQRYFLF
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urease alpha chain [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A;Note: Nostoc sp. PCC 7120

A;Note: Nostoc sp. strain PCC 7120

A;Note: Nostoc sp. strain PCC 7120

C;Accession: AG2264

R;Kaneko, T:, Nakamura, Y:, Wolk, C.P.; Kuritz, T:; Sasamoto, S.; Watanabe, A.; Iriguchi
R;Kaneko, T:; Nakamura, Y:; Wolk, C.P.; Kuritz, T:; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A;Rite: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Accession: AG2264

A;Accession: AG2264

A;Accession: AG2264

A;Accession: AG2264

A;Accession: AG2264

A;Cross-references: UNIPARC:UP100000CE887; GB:BA000019; PIDN:BAB75369.1; PID:g17132803;
A;Gene: alr3670

C;Genetics: alr3670

C;Superfamily: urease, alpha subunit; urease 62K chain homology
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                                                                                                                                                                                           -ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEAL 120
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Matches 349; Conserv
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Cipacession: C75586
Riwhite, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; I., M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Mai, S.; Smith, H.O.; Vanter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A.Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Residues: L568 «WHI>
A;Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKMN 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 STNPTMPFTVNTIHEHLDMLMVCHHLSPRIPEDVHFAESRIRPETIAAEDVLHDLGVFSM 360
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
C;Accession: C75586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 --PDENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 MSSDSQAMGRVGEVITRTWQAAHKMKVQRGPLAAPDGR-ADNFRARRYVAKYTINPAIAHG
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C;Superfamily: urease, alpha subunit; urease 62K chain homology
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                                                                                                                           - Deinococcus radiodurans (strain R1)
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                                                                                                                                                                                                                                                                                                                                 Cispecies: Pseudomonas aeruginosa
Ristover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 999-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathor A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83037
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-566 <STO>
A;Crose-references: UNIPARC:UPI0000CSE4A; GB:AE004900; GB:AE004091; NID:g9951134; PIDN: A;Experimental source: strain PA01
C;Genetics:
A;Gene: ureC; PA4868
C;Superfamily: urease, alpha subunit; urease 62K chain homology
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Best Local Similarity 59.2%; Pred. No. 2.6e-123;
Matches 336; Conservative 88; Mismatches 142;
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Matches 339; Conservative
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NiAlternate names: urease alpha chain
C;Species: Haemophilus influenzae
C;Date: 18-Mag-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C;Accession: H64075
C;Accession: H64075
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kalley, J.M.; Weidman, J.D.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Accession: H64075
A;Accession: H6407
                                                                                                                                                                                                                                                                                                                                                                                         GB:L42023; NID:915
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 NIHRMIRAAEEYSMNVGFIGKGNSSSKKQLVEQVEAGAIGFKIHEDWGTTPSAIDHCLSV 236
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N;Alternate names: urea amidohydrolase; urease alpha chain; urease chain C
C;Species: Klebsiella pneumoniae
C;Date: 30-Nov-1990 #sequence_revision 02-Dec-1994 #text_change 05-Oct-2004
C;Accession: C36138
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A;Cross-references: UNIPROT:P44391; UNIPARC:UPI0000137D6B; GB:U32736;
C;Superfamily: urease, alpha subunit; urease 62K chain homology
C;Keywords: hydrolase; metalloprotesin; nickel
F;5-555/Domain: urease 62K chain homology <UG2>
F;141,143,224,367/Binding site: nickel 2 (His, His, Lys, Asp) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.9%; Score 1826; DB 2; Length 58.9%; Pred. No. 7.2e-123;
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C;Superfamily: urease, alpha subunit; urease 62K chain homology
F;2-567/Product: urease 62K chain #status experimental <a href="MAIN">MAIN</a>
F;4-550/Domain: urease 62K chain meatus experimental <a href="MAIN">MAIN</a>
F;134,136,217,360/Binding site: nickel 2 (His, His, His, Asp) #status experimental
F;217,246,272/Binding site: nickel 1 (Lys, His, His) #status experimental
F;217/Binding site: carbon dioxide (Lys) (covalent) (by urease activase) #status experimental
F;219,320/Active site: His #status experimental
                                                                   accessory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: Structures of the Klebsiella aerogenes urease apoenzyme and two active-site 1
A;Reference number: A58580; MUID:96146054; PMID:8718850
A;Contents: annotation; X-ray crystallography, 2.3 angstroms; active site mutagenesis
                                                                                                                                                                                                                       PIDN: AAA25151.1;
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R;Mulrooney, S.B.; Hausinger, R.P.
J. Bacteriol. 172, 5837-5843, 1990
A;Title: Sequence of the Klebsiella aerogenes urease genes and evidence for A;Areference number: A36138; MUID:91008957; PMID:2211515
A;Accession: C36138
A;Molecule type: DNA
A;Residues: 1-567 <MUL>
A;Cross-references: UNIPARC:UPI00001120E5; GB:M36068; NID:g149335; PIDN:AAA2
B;Jabri, E.; Karplus, P.A.
submitted to the Brookhaven Protein Data Bank, June 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ureC
C;Complex: trimer of heterotrimeric subunits consisting of 11K (gamma), 12K
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                                                                                                                                                                                                                                                                                                          A,Reference number: A65977; PDB:1KRA
A;Contents: annotation; X-ray crystallography, 2.3 angstroms, R;Dabri, E.; Carr, M.B.; Hausinger, R.P.; Karplus, P.A.
Science 268, 998-1004, 1995
A;Title: The crystal structure of urease from Klebsiella aerc
A;Reference number: A56340; MUID:95273988; PMID:7754395
A;Contents: annotation; X-ray crystallography, 2.3 angstroms
Biochemistry 35, 10616-10626, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84; Mismatches 141;
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A, Description: catalyzes the hydrolysis of one molecule of urea to carbon dioxide and two C, Superfamily: urease, alpha subunit; urease 62K chain homology C, Keywords: heterotrimer; hydrolase; metalloprotein; nickel F; 4550/Domain: urease 62K chain homology <406.7
F; 136, 217, 360/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted F; 217, 246, 272/Binding site: nickel 1 (Lys, His, His) #status predicted F; 217/Binding site: aloon dioxide (Lys) (covalent) (by urease activase) #status predicter F; 219, 320/Active site: His #status predicted
                                                                                                                                                                                                                                                                                                             comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: ureC
C;Complex: trimer of heterotrimeric subunits consisting of 11K (gamma), 12K (beta), and
C;Function:
                                                                                                                                                                                                                                                                                                                             A;Accession: D43719
A;Accession: D43719
A;Molecule type: DNA
A;Residus: 1-567 <JON>
A;COSS-references: UNIPROT:P17086; UNIPARC:UPI0000137D74; GB:M31834; NID:g150914;
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 RAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYDV
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59.5%; Pred. No. 6.1e-122;
ive 91; Mismatches 136; Indels
                                                                                                                        urease (EC 3.5.1.5) 62K chain - Proteus mirabilis
N;Alternate names: urease alpha chain
C;Species: Proteus mirabilis
C;Date: 03-Mar-1993 #sequence_revision 02-Dec-1994 #text
C;Accession: D43719
R;Jones, B.D.; Mobley, H.L.T.
J. Bacteriol. 171, 6414-6422, 1989
A;Title: Proteus mirabilis urease: nucleotide sequence ô
A;Reference number: A43719; MUID:90078080; PMID:2687233
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  ETYEVRADGELLTCEPATVLPMAORYFLF
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Best Local Similarity 59.5%
Matches 337; Conservative
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A;Recession: S45607
A;Accession: S45607
A;Accession: S45607
A;Accession: S45607
A;Accession: S4607
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A;Accession: S4607
A;Accession: S4607
A;Accession: Number S4007
A;Accession: Number S4007
A;Accession: Number S4007
A;Genetics:
A;Ge
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                                                                                                                                                                                                                                                     urease (EC 3.5.1.5) - Rhizobium meliloti
C;Species: Rhizobium meliloti
C;Species: S-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: S42607
R;Miksch, G; Arnold, W; Lentzsch, P.; Priefer, U.B.; Puehler, A.
Mol. Genet. 242, 539-550, 1994
A;Title: A 4.6 kb DNA region of Rhizobium meliloti involved in determining urease
ing frames.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 YIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGH 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 AĞEĞKIVTAĞĞMDSHIHFICPQQIEEALMSĞLTÇMLĞĞĞTĞPAHĞTLATTÇTPĞPWHIAR 181
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Pred. No. 1.4e-122;
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59.8%;
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Best Local Similarity 59.8
Matches 340; Conservative
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542 IVKADGVPLVCEPATELPMAQRYFLF
                                                                      Search completed: November 28, 2005, Job time: 38.4836 secs
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                                                                                                                    Substance names: urease alpha chain - Proteus vulgaris

N;Alternate names: urease alpha chain
C;Species: Proteus vulgaris
C;Date: 29-Jan-1993 #sequence_revision 02-Dec-1994 #text_change 05-Oct-2004
C;Accession: S08480
R;Mocrsdorf, G; Kaltwasser, H.
FEMS Microbiol. Lett. 66, 67-74, 1991
A;Title: Cloning of the genes encoding urease from Proteus vulgaris and sequencing of the A;Reference number: S08478; MUID:92038908; PMID:1936938
A;Recession: S08478; MUID:92038908; PMID:1936938
A;Recession: S08480
A;Recession: S08480
A;Recession: S08480
A;Recession: S08478; MUID:92038908; PMID:1936938
A;Recession: S08480
A;Recession: S08478
A;Recess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEYI 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 ECVDVLITNAIIIDHWGIVKADIGIKDGRITGIGKAGNPDVQPNVD--1VIGPGTEVVAG 121
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Pred. No. 1.2e-121;
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RA MEDIINE=22540238; PubMed=12652903; DOI=10.1080/1042517021000039230;

RA MEDIINE=22540228; PubMed=12652903; DOI=10.1080/1042517021000039230;

RA MEDIINE=22540228; PubMed=12652903; DOI=10.1080/1042517021000039230;

RA MEDIINE=22540228; PubMed=12652903; DOI=10.1080/104251702100003929;

RA MEDIINE=22540228; PubMed=2.F.;

RA MCDONOUGH P. MCDONOUGH S.; Chang Y.F.;

RY Gene Cluster.",

DNA Seq. 13:321-331(2002).

RHSP; PH9417; LESY.

DN RSP; PH9417; LESY.

DN RSP; PH9417; LESY.

DN RSP; PH9417; LESY.

DN RO; GO:0016787; F:nickel ion binding; IEA.

DN RO; GO:0016787; F:nickel ion binding; IEA.

DN RO; GO:0016787; F:nickel ion binding; IEA.

DN RO; GO:0016893; F:urease activity; IEA.

DN RO; GO:0006807; P:nitrogen compound metabolism; IEA.

DN RINEPPO; IPR001894; Urease alpha.

DN Refam; PF00449; Urease alpha.

DN PROSITE; PS001120; Urease alpha.

PROSITE; PS001120; UREASE 1; 1.

DN ROSITE; PS001120; UREASE 1; 1.

DN ROSITE; PS001120; UREASE 2; 1.

SRQUENCE S69 AA; 61922 MM; 33938FFC83EC39E26 CRC64;
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                                                 LRAABEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                              VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
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GO: GO: 0016151; F: nickel ion binding; IEA.
GO: GO: 0009039; F: nitraese activity; IEA.
GO: GO: 00008039; F: nitraese activity; IEA.
GO: GO: 00008039; F: nitraese activity; IEA.
InterPro; IPR006680; Amidohydro 1.
InterPro; IPR0068848; Urease alpha.
InterPro; IPR008848; Urease alpha.
InterPro; IPR008295; Urease alpha.
InterPro; IPR011612; Urease alpha.
InterPro; IPR011612; Urease alpha.
InterPro; IPR0101612; Urease alpha.
InterPro; IPR010126; Urease alpha; 1.
PIRSF; PIRSF001226; Urease alpha; 1.
PIRSF; PIRSF001226; Urease alpha; 1.
PROSITE; PS01120; UREASE 1; 1.
PROSITE; PS01120; UREASE 2; 1.
SEQUENCE 569 AA; 61670 MW; 4C96852826C7A784 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           76.7%; Score 2301; DB 2; Length 5 73.5%; Pred. No. 3.4e-149; Live 75; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRANT=MEL-HP27;
Duan G.C., Dai L.P.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AR259685; AR551176.1; -; Genomic_DNA.
HSSP; P1491; 1E9Y.
GO; GO:0016787; F:hydrolase activity; IEA.
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Last annotation update)
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Matches 417; Conservative
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01-OCT-2003
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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"Molecular analysis of urease genes from a newly identified uncultured
species of Helicobacter.";
Infect. Immun. 62:1631-1638(1994).
VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
                                                                                                                                                                                                                                                                                         243 VQVAIHTDTLNEAGCVEDTWAAIAGRTMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP
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                                                                                                                                                                                                LRAABEYSMINGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
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Helicobacteraceae, Helicobacter.
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-!- CATALYTIC ACTIVITY: Urea + H(2)0 = CO(2) + 2 NH(3).

-!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).

-!- SUBUNIT: Consists of two subunits (alpha and beta).

-!- FTW: Lys-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).

-!- SIMILARITY: Belongs to the urease family.

-!- CAUTION: In Helicobacter the beta subunit is what is known in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NCV-1995 (Rel. 32, Created)
01-NCV-1995 (Rel. 32, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Urasae beta subunit (EC 3.5.1.5) (Grea amidohydrolase)
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543 YHVFVDGKEVTSKPATKVSLAQLFSIF
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NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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                                                                                                                                                                                                                                                                    Length 568;
                                                                                                                                                                 Proton donor (By similarity).
Nickel 2 (By similarity).
Nickel 2 (By similarity).
Nickel 1 and 2 (By similarity).
Nickel 1 (By similarity).
Nickel 1 (By similarity).
Nickel 2 (By similarity).
Nickel 2 (By similarity).
Substrate (By similarity).
Substrate (By similarity).
Substrate (By similarity).
W; E2C036DF30377917 CRC64;
                                                                                                                                                                                                                                                                 Score 2298.5; DB 1; Length
Pred. No. 5e-149;
74; Mismatches 74; Indels
                                            InterPro; IRR006680; Amidohydro 1.
InterPro; IRR006680; Urease_alpha.
InterPro; IRR001612; Urease_alpha.
InterPro; IRR001612; Urease_alpha N.
InterPro; IRR008295; Urease_alpha N.
Pfam; PF00449; Urease_alpha; 1.
PRSF; PR01972; Urease_alpha; 1.
PRNYS; PR01972; Urease_alpha; 1.
PROSITE; P801120; UREASE_1; 1.
PROSITE; P800145; UREASE_1; 1.
Hydrolase; Metal-binding; Nickel.
ACT_SITE
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                            EMBL; L25079; AAA65723.1; -; Genomic_DNA
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nes 418; Conservative
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219
248
                                       HSSP; P14917; 1E9Z
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                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDLINE=99120557; PubMed=9923682; DOI=10.1038/16495;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., dealonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
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Nature 397:176-180(1999).
                                                                                                                                                                                               Helicobacter pylori 199 (Campylobacter pylori 199).

Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales;
Helicobacteraceae, Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).

PTM: Lys-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).

MISCELLANEOUS: Oligomerization may protect the enzyme against denaturation in an acidic environment (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
-!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
-!- SUBUNIT: Heterohexamer of 3 alpha and 3 beta subunits. Four heterohexamers assemble to form a 16 nm spherical complex (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Belongs to the urease family.

CAUTION: In Helicobacter the beta subunit is what is known in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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Nickel 2 (By similarity).
Nickel 1 and 2 (By similarity).
Nickel 1 and 2 (By similarity).
Nickel 1 (By similarity).
Nickel 1 (By similarity).
Nickel 2 (By similarity).
Substrate (By similarity).
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                                                 01-APR-1990 (Rel. 14, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Urease beta subunit (EC 3.5.1.5) (Urea amidohydrolase).
Name-ureB; Synonyms-hpuB; OrderedlocusNames-
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PIR; B38537; URKCBP.
InterPro; IPR006680; Amidohydro_1.
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PRIRS; PRSF001226; Urease alpha; 1.
PRINTS; PRO1752; UREASE ITGREAMS; TIGRO1792; UREASE alph; 1.
PROSITE; PS01120; UREASE 1; 1.
PROSITE; PS01120; UREASE 2; 1.
Complete proteome; Hydrolase; Metal-bir ACT SITE
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InterPro; IPR011612; Urease alpha N.
InterPro; IPR008295; Urease alphaIone.
Pfam; PP01979; Amidohydro 1; 1.
Pfam; PF00449; Urease alpha; 1.
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URE2 HELPJ
P69997; P14917;
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        ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
                                                                                                                     VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSSTTP 301
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                                                                                                                                                                                                       SQAMGRVGEVITRIWQTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEY
                                             GEGMI ITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM
                                                                                LRAABEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
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                                                                                                                                                                                                                                                                              P69956; P14917; QPR3B3; 01-ARR-1990 (Rel. 14, Created) 01-MAY-1992 (Rel. 22, Last sequence update) 01-MAY-1905 (Rel. 24, Last annotation update) Urease beta subunit (BC 3.5.1.5) (Urea amidohydrolase). Name-aurea; Synonyma-lpulB, OrderedLocusNames-HP0072; Helicobacter pylori (Campylobacter pylori). Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clayton C.L., Pallen M.J., Kleanthous H., Wren B.W., Tabaqchali S., "Nucleotide sequence of two genes from Helicobacter pylori encoding
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NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
MEDIAINE=97394467; Pubded=9222185; DOI=10.1038/41483;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
                                                                                                                                                                                                                                                                                                                                                                          569 AA
                                                                                                                                                                                                                                                                                                        FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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NCBI_TaxID=210;
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STRAIN=85P;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
        ness E.F.,
Khalak H.G.,
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PUDMAG=1887197; DOI=10.1016/0882-4010(91)90062-F;
Evans D.J. Jr., Evans D.C., Kirkpatrick S.S., Graham D.Y.,
"Characterization of the Helicobacter pylori urease and purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS), AND SUBUNIT STRUCTURE. PubMed=1137317; DOI=10.1038/88563, Lee M.H., Oh B.-H.; HA N.-C., Oh S.-T., Sung J.Y., Cha K.A., Lee M.H., Oh B.-H.; "Supramolecular assembly and acid resistance of Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genes in Escherichia coli
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-1- SUBUNIT: Heterohexamer of 3 alpha and 3 beta subunits. Four heterohexamers assemble to form a 16 nm spherical complex.
-1- PTM: Ly8-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).
-1- MISCELLANBOUS: Oligomerization may protect the enzyme against denaturation in an acidic environment.
-1- SIMILARITY: Belongs to the urease family.
-1- SAUTION: In Helicobacter the beta subunit is what is known in other bacteria as the alpha subunit.
Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F. Peterson S.M., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H. Glodek A., McKehney K., FitzGerald L.W., Lee N., Adams M.D., Hickey B.K., Berg D.E., Gocayne J.D., Unterback T.R., Peterson J.D. Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C. Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Praser C.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hu L.T., Mobley H.L.T.; "Purification and N-terminal analysis of urease from Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dunn B.E., Campbell G.P., Perez-Perez G.I., Blaser M.J.; "Purification and characterization of urease from Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Turbett G.R., Hoej P.B., Horne R., Mee B.J.; "Purification and characterization of the urease enzymes of Helicobacter species from humans and animals.";
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--- COFATOR: Binds 2 nickel ions per subunit.
--- BIOPHYSICOCHEMICAL PROPERTIES:
Kinetic parameters:
Km0.48 mM for urea;
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"Expression of Helicobacter pylori urease ge
grown under nitrogen-limiting conditions.";
Bacteriol. 174:2466-2473(1992).
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MEDLINE=92210488; PubMed=1313413;
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MEDLINE=90202165; PubMed=2318539;
Hu L.T., Mobley H.L.T.;
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                                                                                                                                                                                                                                                                                                                                                          Nature 388:539-547(1997).
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ilarity 73.4%; Pred. No. 6.3e-149;
Conservative 76; Mismatches 75;
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  European Bioinformatics Institute. There are no restrictions on as long as its content is in no way modified and this statement is
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Matches 415; Conserv
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PubMed=15052678;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNPRIKRYLSKYTINPA1AHGISEY 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                        MEDLINE=20305050; PubMed=10844692; Akada M., Nakazawa T., Akada J.K., Shirah M., Takeuchi H., Tsuda M., Nakazawa T., Iakeuchi H., Tsuda M., Nakazawa T., Iadentification of the urease operon in Helicobacter pylori and its control by mRNA decay in response to pH."; Mol. Microbiol. 36:1071-1084(2000). EMBL; ABA84533:1; -; Genomic_DNA.
                                                                     Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                       GO, GO:0016787; F:hydrolase activity; IEA.
GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0009019; F:nickel ion binding; IEA.
GO; GO:0009019; F:nitrogen compound metabolism; IEA.
GO; GO:0006807; P:nitrogen compound metabolism; IEA.
InterPro; IPR006809; Amidohydro 1.
InterPro; IPR008295; Urease_alpha.
InterPro; IPR01612; Urease_alpha.
Pfam; PF01979; Amidohydro 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1752; UREASE.
TIGREAMS; TIGR01792; urease alph; 1.
PROSITE; PS01120; UREASE 1; 1.
PROSITE; PS010145; UREASE 2; 1.
SEQUENCE 569 AA; 61670 MW; 4C8A6BDA3A295584 CRC64;
  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                               NCBI_TaxID=210;
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63 NTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALAG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Turnection of prokaryotic expression system of ureB gene from a "Construction of prokaryotic expression system of ureB gene from a clinical Helicobacter pylori strain and identification of the recombinant protein immunity.";

If world J. Gastroenterol. 10:977-984 (2004).

R MBL; AY714224; AAU21200.1; -; Genomic DNA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016787; F:hydrolase activity; IEA.

GO; GO:0016151; F:nickel ion binding; IEA.

GO; GO:00169039; F:urease activity; IEA.

GO; GO:0006807; P:nitrogen compound metabolism; IEA.

InterPro; IPR005648; Urease_alpha.

InterPro; IPR01502; Urease_alpha.

InterPro; IPR011612; Urease_alpha.

Pfam; PF01979; Manidohydro_1; 1.

Pfam; PF01979; Urease_alpha; 1.

PRINTS; PR01752; UREASE.

R TIGRPAMS; TIGRN01792; UREASE.

R PROSITE; PS01120; UREASE 1; 1.

R PROSITE; PS01145; UREASE 1; 1.

R PROSITE; PS01144 MW; IDFA1AAS96205A9C CRC64;
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Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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Last annotation update)
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                                                                                                                                                                                        567 AA
Created)
                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                                                                     Q64EY3_HELPY PRELIMINARY;
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ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
                                             3 KISRKEYVSMYGPTTGDKVRLGDTDLIAEVEHDYTIYGEELKFGGGKTLREGMSQSNNPS
243 VQVAIHTDTLNEAGCVEDTMAAIAGRTMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP
                             TIPYTINTVAEHLDMLMTCHHLDKRIREDLOFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                       SQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                    422 IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                                                                                                                              482 GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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Bacteria, Proteobacteria, Epsilonproteobacteria, Campylobacterales,
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Karini Arzenani M., Mohammadi M.;
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY227442; AAO34403.1; -; Genomic_DNA.
HSSP; P14917; 1E9Y.
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H35/; F143/1) LD3...
H35/; G0:0016789; F:hydrolase activity; IEA.
G0; G0:00016151; F:hydrolase ion binding; IEA.
G0; G0:00009039; F:urease activity; IEA.
G0; G0:0006807; P:nitrogen compound metabolism; IEA.
InterPro; IPR006880; Amidohydro_1.
InterPro; IPR005848; Urease alpha.
InterPro; IPR01612; Urease alpha.
Pfam; PF01979; Amidohydro_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               76.3%; Score 2288; DB 2; 73.2%; Pred. No. 2.6e-148; ive 75; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                    569 AA
                                                                                                                                                                                                                                                                           542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                             : |||||| |:: | || :: | XHVFVDGKEVTSKPANKVSLAQLFSIF 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRESF, PIRSF001226; Urease_alpha; 1. PRINTS; PRO1753; UREASE.
TIGRNAMS; TIGR01793; urease_alph; 1. PROSITE; PS01120; UREASE 1; 1. PROSITE; PS00145; UREASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicobacteraceae; Helicobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01979; Amidohydro l
Pfam; PF00449; Urease alpha
                                                                                                                                                                                                                                                                                                                                                                                 Q84F75 HELPY PRELIMINARY;
Q84F75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Simines 415;
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                               302
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KAKYDANITFVSQAAYDKGIKEELGLERQVLPVKNCRNITKKDMQFNDTTAHIEVNPETY 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              242
                                              GSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHHG 482
                                                                KAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKTF 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSSTTP 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Helicobacter pylori (Campylobacter pylori).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerold A., Simpson K., Chang Y.-F.;
Submitted (PEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF352376; AAK32714.1; -; Genomic_DNA.
HSSP; P1991'; 1B9Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0016787; F:Bydrolase activity; IEA.
GO; GO:0016191; F:nickel ion binding; IEA.
GO; GO:0009039; F:urease activity; IEA.
GO; GO:0009039; F:urease activity; IEA.
GO; GO:0006807; F:nitrogen compound metabolism; IEA.
InterPro; IPR006680; Amidohydrol.
InterPro; IPR006895; Urease alpha.
InterPro; IPR001895; Urease alpha.
InterPro; IPR011612; Urease alpha.
Pfam; PF01979; Amidohydrol; 1.
Pfam; PF01979; Urease alpha; 1.
PINSF; PINSF01226; Urease alpha; 1.
PINSF; PINSF01226; Urease alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS, TIGRO1792; urease alph; 1.
PROSITE; PS01120; UREASE 1; 1.
PROSITE; PS00145; UREASE 2; 1.
SEQUENCE 569 AA; 61713 MW; C243ABC38C25D187 CRC64;
                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.4%; Score 2291; DB 2; 73.2%; Pred. No. 1.6e-148; ive 76; Mismatches 76;
                                                                                                                                                                                                                                                                              569 AA
                                                                                                                                                                       543 EVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                     Q9AFB1 HELPY PRELIMINARY;
Q9AFB1;
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NUCLEOTIDE SEQUENCE.
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Best Local Similarity
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GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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URE2 HELFE
1D CRE2 HELFE
1D CRE2 OBS18;
AC 008716; QSR3B3;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 47, Last annotation update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OC
                                                                                                                                                                                                                                                                                                                                                               049CA0F87E2CABID CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 75.1%; Score 2251; DB 2; Best Local Similarity 73.9%; Pred. No. 8.8e-146; Matches 407; Conservative 72; Mismatches 72;
InterPro; IPR006680; Amidohydro 1.
InterPro; IPR008848; Urease_alpha.
InterPro; IPR01848; Urease_alpha.
InterPro; IPR011612; Urease_alpha.
Pfam; PF01979; Amidohydro 1; 1.
Pfam; PF00449; Urease_alpha; 1.
PINSF; PINSF001226; Urease_alpha; 1.
PRNTS; PR01752; UREASE.
TIGRPAMS; TIGR01792; urease_alph; 1.
PROSITE; PS01120; UREASE 1; 1.
SEQUENCE 559 AA; 60607 MW; 049CA0F871
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YHVFVDGKEVT
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         GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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STRAIN=CH-CTX1.

NUCLECTIDE SEQUENCE.

STRAIN=CH-CTX3532; PubMed=10660136;

Opazo P., Muller I., Rollan A., Valenzuela P., Yudelevich A.,

Garcia-de la Guarda R., Urra S., Venegas A.,

"Serological response to Helicobacter pylori recombinant antigens in

Chilean infected patients with duodenal ulcer, non-ulcer dyspepsia and

gastric cancer.";
                                                                                                                                                                      VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGGHSPDVITWAGELNILPSSTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243 VQVAIHTDTLNEAGCVKDTMAAIAGRTMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIPYTINTVAEHLDMLMTCHHLDKRIREDLOFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                       |||:|:|||||||:||| GEGLIVTAGGIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRRNLKMM
                                                                                                                                    LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
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MEDLINE=2121498; PubMed=12125208;
Muller I., Madina-Selby A., Palacios J.L., Martinez P., Opazo P.,
Muller I., Madina-Selby A., Palacios J.L., Martinez P., Opazo P.,
Muller I., Mancilla M., Valenzuela P., Yudelevich A., Venegas A.;
"Cloning and comparison of ten gene sequences of a Chilean H. pylori
strain with tother H. pylori strains revealed higher variability for
Biol. Res. 35:67-84(2002)
EMBL, AR479026; AAL86896.1; -; Genomic_DNA.
HSSP, P14917; 1E93.
SMR; Q8RNU6; 1-553.
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Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
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GO:0016787; F:hydrolase activity; IEA.
GO:0016151; F:nickel ion binding; IEA.
GO:0009039; F:urease activity; IEA.
GO:0006807; P:nitrogen compound metabolism; IEA.
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Last annotation update)
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543 YRVFVDGKEVTSKPANKVSLAQLFSIF
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01-JUN-2002 (TrEMBLrel. 21,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QBRNUG HELPY PRELIMINARY;
QBRNUG;
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NUCLEOTIDE SEQUENCE
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361

362 421 422 481

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Infect. Immun. 69:5914-5920(2001)
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                                                                                                                                                                                                                                                                       This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                   Helicobacter species from humans and animals.";
Infect. Immun. 60:5259-526(1992).
Infect. Immun. 60:5259-526(1992).
-!- CATALYTIC ACTIVITY: Urea + H(2)0 = CO(2) + 2 NH(3).
-!- COPACTOR: Binds 2 nickel ions per subunit (By similarity).
-!- SUBUNIT: Consists of two subunits (alpha and beta).
-!- PTM: Lys-219 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).
-!- SIMILARITY: Belongs to the urease family.
-!- SIMILARITY: Belongs to the beta subunit is what is known in
                          of Helicobacter felis urease
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o
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Nickel 2 (By similarity).

Nickel 2 (By similarity).

Nickel 1 and 2 (By similarity).

Nickel 1 (By similarity).

Nickel 1 (By similarity).

Nickel 2 (By similarity).

Substrate (By similarity).

Substrate (By similarity).

W, 66DBB99E2CC7CEA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Metal-binding; Nickel.
                                                                                      STRAIN=ATCC 49179;

DubMed=1452359;

Turbett G R., Hooj P.B., Horne R., Mee B.J.;

"Purification and characterization of the urease enzymes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74.8%; Score 2244; DB 1; 72.5%; Pred. No. 2.7e-145; ive 71; Mismatches 85;
                                                                                                                                                                                                                                                                                                                                                           PIR; C49215; C49215.
PIR; S35291; S35291.
HSSP, PIRJ1; 1E92.
InterPro; IPR006680; Amidohydro 1.
InterPro; IPR006848; Urease_alpha.
InterPro; IPR001612; Urease_alpha.
InterPro; IPR008295; Urease_alpha N.
Pfam; PF01979; Amidohydro 1; 1.
Pfam; PF00449; Urease_alpha; 1.
PRINFS; PR01752; Urease_alpha; 1.
PRINFS; PR01752; Urease_alpha; 1.
TIGRFPAMS; TIGR01792; urease_alph; 1.
                                                                                                                                                                                                                                                    other bacteria as the alpha subunit.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct protein sequencing; Hydrolase;
ACT_SITE 322 322 Proton do
MEDLINE=94018627; PubMed=8412683;
Ferrero R.L., Labigne A.;
"Cloning, expression and sequencing
                                                  Mol. Microbiol. 9:323-333(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS01120; UREASE 1; 1. PROSITE; PS00145; UREASE 2; 1.
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PROTEIN SEQUENCE OF 1-12
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569 AA;
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XX MEDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;

AN EDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;

AN EDLINE=22709201; PubMed=12810954; DOI=10.1073/pnas.1332093100;

Bell M., Droege M., Fartman B., Fischer H.-P., Ge Z., Hoerster A.,

A Holland R., Klein K., Koenig J., Macko L., Mendz G.L., Nyakatura G.,

Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;

The complete genome sequence of the carcinogenic bacterium

The complete genome sequence of the carcinogenic bacterium

The complete genome sequence of the carcinogenic bacterium

R Hisobacter hepaticus.",

R EMBL, AR332656; AAK69199.1; -; Genomic_DNA.

R EMBL, AB4917; ISBY.

R HSSP; P18314; 1A5N.

R SMR, Q9984; 1-569.
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MEDINE=21391660; PubMed=11500473;
DOI=10.1128/IAI.69-9.5914-5920.2001;
BOCKWith C.S., McGee D.J., Mobley H.L.T., Riley L.K.;
"Cloning, expression, and catalytic activity of Helicobacter hepaticus
                                                            243 VQVAIHTDTLNEAGCVEDTLEAIAGRTIHTFHTEGAGGGAAPDVIKAAGEFNILPASTNP
                                                                                                                                                                                                                                                                                                                                        303 TIPFTKATEAEHMDMLAVCHHLDKSIKEDVQFADSRIRPQTIAAEDQLHDMGIFSITSSD
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Helicobacteraceae; Helicobacter.
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GO; GO:0016151; F:nickel ion binding; IEA.
GO; GO:0008019; F:nitrase activity; IEA.
GO; GO:0008007; F:nitragen compound metabolism; IEA.
InterPro; IPR006809; Amidohydro 1.
InterPro; IPR001612; Urease_alpha.
InterPro; IPR011612; Urease_alpha.
Pfam; PF01979; Amidohydro 1; 1.
Pfam; PF01979; Amidohydro 1; 1.
PRINTS; PR01752; UREASE.
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362 3
221 2
569 AA;
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nes 375; Conserv
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                                                                569 AA; 61510 MW; 2825D1E6406F6429 CRC64;
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; Pred. No. 6.9e-136;
82; Mismatches 100;
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TIGRFAMS; TIGR01792; urease_alph;
PROSITE; PS01120; UREASE 1; 1.
PROSITE; PS00145; UREASE_2; 1.
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DT 13-0CT-
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatios and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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PTM: Lys-219 is carbamylated. The carbamoyl group provides the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
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322 322 Proton donor (By similarity).
136 Nickel 2 (By similarity).
139 Nickel 1 (By similarity).
248 248 Nickel 1 and 2 (By similarity).
274 274 Nickel 1 (By similarity).
275 Nickel 1 (By similarity).
276 Nickel 2 (By similarity).
277 Substrate (By similarity).
278 Substrate (By similarity).
279 Substrate (By similarity).
270 Substrate (By similarity).
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                                             ligands for the two nickel ions (By similarity) SIMILARITY: Belongs to the urease family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .7e-130;
es 112;
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66.1%; Pred. No. 1.7e-
tive 77; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; D14439; BAA03325.1; -; Genomic_DNA
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HSSP, P18314; IEJX.
InterPro; IPR016680; Amidohydro 1.
InterPro; IPR011550; Amidohydro like.
InterPro; IPR01151; Urease alpha.
InterPro; IPR011612; Urease alpha N.
InterPro; IPR01295; Urease alpha InterPro; IPR01295; Urease alphalone.
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RX STRAINE-98044033; PubMed-9384377; DOI=10.1038/36786;
Kunst F., Ogassawara N., Moszer I., Albertini A.M., Alloni G.,
Kunst F., Ogassawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Bartero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Azevedo V., Barter L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Browillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Browillet S., K., Codani J. J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Choi S.-K., Codani J. J., Fune S., Galizzi A., Galieron P.T.,
RA Fritz C., Fujita M., Fujita Y., Fune S., Galizzi A., Galieron N.,
RA Fritz C., Fujita M., Fujita Y., Fune S., Galizzi A., Galieron N.,
RA Guiseppi G., Guy B.J., Hagag K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.-F., Itaya M.,
Alones L.-M., Joris B., Karamata D., Kasaharar Y., Klaerr-Blanchard M.,
RA Jones L.-M., Joris B., Karamata D., Kasaharar Y., Klaerr-Blanchard M.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Mauel C.,
Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
Scoffone F., Sekiguchi J., Sakwaka A., Serror S., Serror P.,
Scoffone F., Sekiguchi J., Sakwaka A., Tarconi E., Takagi T., Tarahashi H.,
RA Takemaru K., Takeuchil M., Tamakoshi A., Tarnaka T., Terpstra P.,
Tognoni A., Tosato V., Uchiyama S., Vandeler B., Wedler E.,
Vassarotti A., Viari A., Wambutt R., Wamler E., Wedler E.,
Vassarotti A., Viari A., Wambutt R., Yamamoto H., Yamane K.,
Vassarotti A., Viari A., Wambutt R., Yamamoto H., Yamane K.,
                                                                                                                                                                                                                       418 VSEYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREM 477
                     239 EYDVQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSS
                                                                         TTPTIPYIPYTINTVAEHLDML/MTCHHLDKRIREDLOFSOSRIRPGSIAAEDVLHDMGVIAMT
                                                                                                                                                359 SSDSQAMGRAGEVIPRTWQTADKNKKEFGKLPED-GKDNDNFRIKRYISKYTINPALTHG
                                                                                                                                                                                                                                                                                                FGHHGKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAY-2005 (Rel. 47, Last annotation update)
Urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase).
Name-ureC; OrderedLocusNames=BSU36640;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Bacillales, Bacillaceae, Bacillus.
NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=168;
Glaser P., Cruz H., Danchin A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                           538 DPKTFEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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NUCLEOTIDE SEQUENCE.
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                     181 ERMLEAADAFPUNLGFLGKGNASTPAPLREQIEAGAIGLKLHEDWGTTPAAIRTCLSVAD 240
GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 ALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 HRMLRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVAD 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
EMBL; BA000004; BAB03973.1; -; Genomic_DNA.
PIR; F83681; F83681.
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                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=C-125 / JCM 9153;
MEDLINE-20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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                                                                                                                                                                                                                                                                                                                                                      Bacteria, Firmicutes; Bacillales; Bacillaceae; Bacillus
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                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P41020; 1UBP.
SMR; Q9KG59; 1-571.
G0; G0:0016787; F:nickel ion binding; IEA.
G0; G0:0016151; F:nickel ion binding; IEA.
G0; G0:0019039; F:urease activity; IEA.
G0; G0:0019627; P:urease activity; IEA.
InterPro; IPR006680; Amidohydro_1.
InterPro; IPR005848; Urease_alpha.
InterPro; IPR008295; Urease_alpha.
InterPro; IPR01812; Urease_alpha.
InterPro; IPR01812; Urease_alpha.
                                                                                                                                                                                                           571 AA
                                                                                              FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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TIGREAMS; TIGR0179; urease alph; 1. PROSITE; PS01120; UREASE 1; 1. PROSITE; PS00145; UREASE 2; 1.
                                                                                                                                                                                                                                                                                                  Urease alpha subunit (EC 3.5.1.5).
Name=ureC; OrderedLocusNames=BH0254;
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                                                                                                                                                                                                        Q9KG59, BACHD PRELIMINARY; Q9KG59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 368; Conservative
                                                                                                                                                                                                                                                                                                                                          Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTPT1PYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 SPDENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 ALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179 HRMLRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVAD 238
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Yasumoto K., Yata K., Yoshida K., Yoshikawa H.-F., Zumstein E., Yoshikawa H., Danchin A.;
"The complete genome sequence of the Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                    Nature 390:249-256(1997).

-!- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).

-!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).

-!- SUBUNIT: (Alpha, beta, gamma) (3) (By similarity).

-!- PTM: Lys-220 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).

-!- SIMILARITY: Belongs to the urease family.
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Nickel 2 (By similarity).
Nickel 1 (By similarity).
Nickel 1 and 2 (By similarity).
Nickel 1 (By similarity).
Nickel 1 (By similarity).
Nickel 2 (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Substrate (By similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Metal-binding; Nickel
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                                                                                                                                                                                                                                                                                                                    EMBL; Y08559; CAA69859.1; -; Genomic_DNA.
EMBL; Z99122; CAB15681.1; -; Genomic_DNA.
PIR; D69729; D69729.
                                                                                                                                                                                                                                                                                                                                                                 HSSP, D1814; 1FWB.
Subtilist; B31193; urec.
InterPro; IPR005680; Amidohydro 1.
InterPro; IPR005680; Amidohydro 1.
InterPro; IPR005849; Urease_alpha.
InterPro; IPR001151; Urease_alpha.
InterPro; IPR001161; Urease_alpha.
InterPro; IPR00399; Urease_alpha.
Pfam; PF01979; Amidohydro 1; 1.
Pfam; PF001979; Amidohydro 1; 1.
PRMNTS; PRSF001226; Urease_alpha; 1.
PRNNTS; PR01752; UREASE.
FroDom; PD001249; Amidohydro like; 1.
TIGRPAMS; TIGR01792; urease_alpha; 1.
PROSITE; PS001120; UREASE 1; 1.
PROSITE; PS001120; UREASE 1; 1.
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                     SSDSQAMGRAGEVIPRTWQTADKNKKEFGKLP-EDGKDNDNFRIKRYISKYTINPALTHG
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Search completed: November 28, 2005, 08:19:48 Job time : 222.186 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description			Adj58251 UreaseXY	Adj58242 UreaseXY	Adj58248 UreaseXY	Adj58245 UreaseXY	Adq37851 H. bizzoz	Pa	Aaw07194 H. pylori	Aaw98511 H. pylori	Pro	H.	Ads09177 H. pylori		Aeb55116 Hylicobac	Aar74337 Helicobac	Aaw06730 H. felis	Aaw80599 Helicobac	Aar67371 Urease A	Aar13550 B subunit	Adm28644 Helicobac	Aar36387 Urease ga	Abul9714 Protein e	Abu41362 Protein e	Abu21842 Protein e
SUMMARIES	Ω		AD036239	ADJ58251	ADJ58242	ADJ58248	ADJ58245	ADQ37851	AAR04580	AAW07194	AAW98511	ABU30687	ADU05536	ADS09177	AAR67378	AEB55116	AAR74337	AAW06730	AAW80599	AAR67371	AAR13550	ADM28644	AAR36387	ABU19714	ABU41362	ABU21842
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## ALIGNMENTS

immunogenic fragment; antibacterial; Vaccine; Helicobacter felis. Claim 10; SEQ ID NO 3; 76pp; English. ADJ58239 standard; protein; 568 AA. Urease subunit polypeptide Y. 11-JUL-2001; 2001EP-00202666. 17-JUL-2000; 2000EP-00202565. (first entry) Cattoli G; (ALKU ) AKZO NOBEL NV. WPI; 2002-124384/17. Helicobacter felis. N-PSDB; ADJ58237 EP1176192-A2 06-MAY-2004 Kusters JG, 30-JAN-2002 ADJ58239; vaccines 

Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of

The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis is Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an urease Y subunit polypeptide of the invention.

Sequence 568 AA;

Query Match

Length 568; DB 5; 100.0%; Score 2999;

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Novel Helicobacter felis urease X and Y subunit polypeptides, useful in the diagnosis of Helicobacter felis infections and in the preparation of
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Pred. No. 6.6e-251;
4; Mismatches 2;
                                                                                            Disclosure; SEQ ID NO 15; 76pp; English
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Matches 562; Conservative
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                                  Matches 568; Conservative
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N-PSDB; ADJ58249.
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                  Best Local Similarity
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The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis is Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an ureaseXX subunit of the invention.
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The present invention relates to a novel Helicobacter felis urease X and Y subunit polypeptides and immunogenic fragments. The polypeptides are used in the manufacture of vaccines against Helicobacter felis infections and in diagnostic tests to detect antibodies against Helicobacter felis. Helicobacter felis is difficult to grow so it is more convenient to use the expression products of the genes encoding the urease X and Y subunits in the manufacture of vaccines. The present sequence represents an
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Pred. No. 3.7e-249;
5; Mismatches 5;
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                                                           TFEVFVDGKLCTSKPASEVPLAQRYTFF
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98.2%;
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                                                                                                                                                                                                                                                                                                                 immunogenic fragment;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            present invention relates to a novel Helicobacter felis urease X and
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Pred. No. 9.1e-250;
4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 6; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.7%;
                                                                                                                               11-JUL-2001; 2001EP-00202666
                                                                                                                                                                  17-JUL-2000; 2000EP-00202565
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Best Local Similarity 98.6
Matches 560; Conservative
                                                                                                                                                                                                                                           Cattoli G;
                                                                                                                                                                                                        (ALKU ) AKZO NOBEL NV.
                                                                                                                                                                                                                                                                           WPI; 2002-124384/17.
N-PSDB; ADJ58240.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 568 AA;
                                                        EP1176192-A2
                                                                                                                                                                                                                                           Kusters JG,
                                                                                             30-JAN-2002
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Helicobacter bizzozeronii infection;
    Mismatches
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    Conservative
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SIMPSON P
ZHU J.
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                   DVQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYH1EGAGGGHSPDVITMAGELNILPSSTT
                                                                                    PTI PYTINTVAEHLDMLMTCHHLDKRIREDLOFSOSRIRPGSIAAEDVLHDMGVIAMTSS
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Pred. No. 2.8e-217;
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N-PSDB; ADJ58243.
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Novel isolated nucleic acid molecule having urease gene cluster, and

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The invention relates to an isolated nucleic acid molecule conferring on Helicobacter bizzozeronii an ability to produce urease, where the nucleic acid molecule is a urease gene cluster comprising at least one urease estructural gene and at least one urease accessory gene. The nucleic acid molecule is chosen from ureA, ureB, ureE, ureG, ureH and ureI. The invention also relates to an isolated protein encoded by the nucleic acid, a vaccine for preventing onset of disease in mammals infected by H. bizzozeronii comprising a nucleic acid and a carrier, and an isolated cartibody or its binding portion raised against the nucleic acid. The moleic acids proteins and antibodies are useful for vaccinating mammals capainst onset of disease caused by infection of H. bizzozeronii, which involves administering the sequences. The sequences are useful for detecting H. bizzozeronii in a sample of tissue or body fluids which involves providing a nucleic acid as an antigen, providing an uncleotide sequence as a probe in a nucleic acid or hybridisation assay, contacting the sample with the antigen or the probe, and detecting any reaction which indicates that H. bizzozeronii is present in the sample. This sequence represents the H. bizzozeronii ureB
conferring on Helicobacter bizzozeronii ability to produce urease, useful as vaccine for preventing disease in mammals infected by H.bizzozeronii.
                                                                                         Claim 24; SEQ ID NO 5; 40pp; English
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Sequence 569 AA;

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                                                              243 VQVAIHTDTLNEAGCVEDTLQAIAGRTIHTFHTEGAGGGHAPDVIKMSGEFNILPASTNP
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                                                                                                ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA
                                                                                                                                                122 GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM
                                                                                                                                                                                                LRAAEEYSMINVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
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 Length 569;
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77.6%; Score 2326; DB 8;
74.1%; Pred. No. 3.1e-194;
ive 75; Mismatches 72;
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           Local Similarity 74.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleotide sequences encoding Campylobacter pylori-ureaseents - and derived vectors, transformants, protein, antibodies and probes, useful diagnosis, treatment and prevention of infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KWKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The protein can be used for the prodn. of antibodies and to prepare vaccines for the prevention /freatment of C. pylori infections. See AAR04578-81. (Updated on 25-MAR-2003 to correct PA field.) (Updated -OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INSP ) INST PASTEUR.
(INRM ) INSERM INST NAT SANTE & RECH MED.
                                                                                                                                                                                                                                                            Part of protein with urease activity
                              Ä
                              standard; protein; 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Page 34; 47pp; French
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88FR-00013135.
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                                                                                                                                                                                                                                                                                                                              Urease; probe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-OCT-1988;
                                                                                                                                             24-OCT-2003
25-MAR-2003
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Matches 416;
                                                                                                                                                                                                      21-SEP-1990
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                                                                                                           243 VQVAIHTDTLNEAGCVEDTMAAIAGRTWHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP 302
                                                                                                                                                                                                                                                                                                                                                       GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Helicobacter polynucleotides - used to develop products for the diagnosis, prevention and treatment of Helicobacter infections and gastrointestinal diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHPO protein; Helicobacter infection; gastroduodenal disease; gastritis;
                                                                                                                                                                                         LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                       SQAMGRVGEVITRTWQTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEY
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                                                                                                                                                                                                                                                    VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kleanthous H, Al-Garawi A, Miller C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW98511 standard; protein; 569
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97US-00881227.
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N-PSDB; AAX14230.
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Vectors, e.g. pORV314 (see also AAT4351), carrying the gene locus can be used to transform host cells for the large-scale prodn. of recombinant, enzymatically inactive, multimeric urease. The urease complex induces a mucosal immune response that can treat or prevent Helicobacter, esp. H. pylori, gastroduodenal infection. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine for inducing mucosal response to Helicobacter - contg. multimeric urease complex and pref. an antibiotic, anti-secretory agent or bismuth
                                                                                                                                                                                     542
                                                                 481
                                                                                      GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT 541
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Sussman I;
                                                             IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                                                                                    2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
SQAMGRVGEVITRIMQTADKNKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEY
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Bhagat H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76; Mismatches
                                                                                                                                                                                                                             FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                      Urease; ureA gene; ureB gene; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 71-73; 98pp; English.
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                                                                                                                                                                                                                                                                                                                                                                        AAW07194 standard; protein; 569
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95US-00568122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   H. pylori urease B subunit.
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(first entry)
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06-DEC-1995;
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11-FEB-1997
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Best Local Si
Matches 416
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                                                                                                                                                                                        ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
                                                                                                                                                                                                                           GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
                                                                                                                                                                                                                                                                                                                                     TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD 361
                         This sequence represents a Helicobacter pylori GHPO protein of the invention. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroduodenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcer diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for
                                                                                                                                                     61
                                                                                                                                                                  KISRKEYVSMYGPTTGDKVRLGDTDLIAEVEHDYTIYGEELKFGGGKTLREGMSQSNNPS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                        VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
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                                                                                                                                    Gaps
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                                                                                                                 Length 569;
                                                                                                                                    75; Indels
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                                                                                                                Query Match 76.6%; Score 2297; DB 2; Best Local Similarity 73.4%; Pred. No. 1.1e-191; Matches 416; Conservative 76; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
         Page 960-962; 2054pp; English.
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YHVFVDGKEVTSKPANKVSLAQLFSIF
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                                                                                diagnosis
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                                                                                                Sequence 569 AA;
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                                                                               detection and
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the inventor fracter to an interest acts completely any one of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
concleic acid; (2) a host cell containing the vector; (3) an isolated
concleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (4) an antibody capable of specifically binding
contisense nucleic acid; (4) an antibody capable of specifically binding
contiseration; (5) producing the polypeptide; (6) inhibiting callular
contiseration; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
contiseration; (7) identifying a compound that influences the activity of
the gene product or that has an activity against a biological pathway
contiseration; (7) identifying a compound that inhibits proliferation of an
corganism acts; (9) manufacturing an antibiotic; (10) profiling a
corganism acts; (9) manufacturing an antibiotic; (10) profiling a
corganism acts; (9) manufacturing an antibiotic; (10) profiling a
corganism acts; (9) manufacturing an antibiotic; (10) profiling a
corganism; or (11) adentifying the target of a compound that inhibits the
corpound; or an organism. The antisense nucleic acids are useful for
identifying proteins or screening for homologous nucleic acids required
contification of an organism. The antisense nucleic acids required
contification of an organism. The antisense nucleic acids required
contification of an organism. The antisense nucleic acids required
contification of an organism. The antisense nucleic acids required
contification of an organism. The antisense nucleic acids required
continued to the strains is present in a culture molecular for rational
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       screening
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                                                                                                                                                                                                                                                                                                                                                                                                                  Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New antisense nucleic acids, useful for identifying proteins or s
for homologous nucleic acids required for cellular proliferation
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates to an isolated nucleic acid comprising any
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                                                                                                                                                                                                                                                                                                                                                                                                                  Ohlsen KL,
Forsyth RA,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 58611; 1766pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                  dalone C,
Carr GJ.
                                                                                                                      2001US-00948993.
2001US-0342923P.
2002US-00072851.
2002US-0362699P.
21-MAR-2002; 2002WO-US009107
                                                                                                                                                                                                                                                                                                                                                                                                                      Malone
                                                                                                                                                                                                                                                                                                                                     (ELIT-) ELITRA PHARM INC.
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Trawick JD,
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Matches 416; Conserv
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25-OCT-2001;
08-FEB-2002;
06-MAR-2002;
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(including the nucleic acid molecule, hyperimmune serum-reactive antigen
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Matches 416; Conservative
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GEGLIVTAGGIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRRNLKWM 182
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/note= "Immunogenic region. Region specifically claimed
in claim 14"
                                                         VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
                                                                                                                                                                                                       TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
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                                        LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rimmune serum reactive antigens from Helicobacter pylori, e nucleic acid molecules, useful for diagnosing, preventing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 184; 176pp; English.
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YHVFVDGKEVTSKPANKVSLAQLFSIF
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D ADUOSS36
ID ADUOSS
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The invention relates to an isolated nucleic acid molecule encoding hyperimmune serum reactive antigen or its fragment. The composition

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or antibody) is useful for manufacturing a medicament or pharmaceutical preparation (e.g. a vaccine) for treating or preventing H. pylori infections. The antigen or its fragment may also be used for isolating, purifying and/or identifying an interaction pattner of the hyperimmune serum reactive antigen or fragment; for generating a peptide binding to the hyperimmune serum reactive antigen or fragment, where the peptide is selected from anticalines; for manufacturing a functional nucleic acid selected from aptamers and spiegelmers; or for manufacturing a functional ribonucleic acid selected from ribozymes, antisense nucleic acids and spiral antigenic protein.
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                                                                                                                                                                                                                                                                                                             76.6%; Score 2297; DB 8; 73.4%; Pred. No. 1.1e-191; ive 76; Mismatches 75;
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Sequence 569 AA;
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19-NOV-1993;
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22-JUN-1995
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                                                                                                                                                                                                                                                                                        The invention relates to a protein having a specific region of primary structure of the beta-subunit Helicobacter pylori urease, appearing as Structure of the beta-subunit Helicobacter pylori urease, appearing as ADS09176 (amino acids 201-318 of the beta subunit) or a sequence which generates antibodies that suppresses proliferation of H. pylori and which suppresses urease activity of H. pylori by an immune reaction. Also included are a gene which encodes the urease fragment, a transformed cell transformed by introducing the urease fragment, a transformed cell transformed by introducing the gene, an antibody which recognises the urease fragment and transforming a plant by introducing the gene into the plant and making it express. The urease fragment is useful for producing blood serum containing antibodies which suppresses proliferation of H. pylori and which suppresses urease activity of H. pylori which involves immunising a living organism (e.g. a human, cow or hen) with the urease immunishing a living organism (e.g. a human, cow or hen) with the urease transferic and peptic ulcers, gastritis and may be implicated in stomach cancer. The urease enzyme is thought to be responsible for maintaining the bacterium in the acid conditions of the stomach. The present sequence is the H. pylori urease beta subunit from which the
                                                                                                                                                                                                  Protein having specific region of beta-subunit urease of Helicobacter pylori, which generates antibodies that suppress proliferation and urease activity of bacteria, useful for preventing Helicobacter pylori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
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                                                                                                                                 DOKU-) DOKURITSU GYOSEI HOJIN KAGAKU GIJUTSU SH.
[FUKU-) FUKUYAMA RINSHO KENSA CENT KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76.1%; Score 2282; DB 8; 73.1%; Pred. No. 2.2e-190; ive 77; Mismatches 75;
                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 2; 26pp; Japanese.
                                                                                                        28-FEB-2003; 2003JP-00054654.
                                                                             28-FEB-2003; 2003JP-00054654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 73.1
Matches 413; Conservative
 Helicobacter pylori
                                                                                                                                                                        WPI; 2004-665475/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 568 AA;
                          JP2004261080-A.
                                                     24-SEP-2004
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The sequence of the Helicobacter felis urease ureB gene product (given in AAR67371) was compared to ureases of Helicobacter pylori (AAR67378), Proteus mirabilis (AAR67379) and jack bean urease (AAR67380) and regions of homology were identified. (Updated on 25-MAR-2003 to correct PN
542
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                                                                                                                                                                                                        Urease; ureB gene; immunogen; vaccine; diagnostic; Helicobacter felis.
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                                                                                               IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrero R, Thiberge J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INSP ) INST PASTEUR.
(INRM ) INST NAT SANTE & RECH MEDICALE
                                                                                                                                                                                                                                                                            FEVFVDGKLCTSKPTSQVPLAQRYT 566
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YHVFVDGKEVTSKPANKVSLAQLFS
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93WO-EP003259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H. pylori urease ureB.
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les 414; Conserv
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The invention relates to inducing an immune response against Helicobacter in a mammal, comprising mucosally administering to the mammal an attenuated Salmonella vector containing a nucleic acid molecule encoding
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GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       an immune response against Helicobacter in mammals, useful for Helicobacter induced gastroduodenal diseases.
                                                      VQVAIHTDILNEAGCVEDTMAAIAGRIMHTFHTEGAGGGHAPDIIKVAGEHNILPASTNP
                                                                                                                                                                                       SQAMGRVGEVITRIWQTADKXKKEFGRLKEEKGDNDNFRIKRYLSKYTINPAIAHGISEY
                                                                                     VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGHSPDVITMAGELNILPSSTTP
                                                                                                                               TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
                                                                                                                                                                           SOAMGRAGEVIPRIWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                                                                     IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                                                                                                                                                                                                GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
                                           LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pHUR3; vaccine; helicobacter pylori infection; urease; immune stimulation; antibacterial; Immunostimulant; antiulcer; cytostatic; antiinflammatory; gastrointestinal-gen.; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hylicobacter pylori Urase B protein fragment SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptic ulcer; carcinoma
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Helicobacter antigen, and parenterally administering to the mammal a Helicobacter antigen. Also included is an attenuated Salmonella vector comprishing a nucleic acid molecule encoding a Helicobacter antigen. The Helicobacter antigen is a urease, a urease subunit, or its immunogenic fragment (encoded by the ureA and ureB genes). The mammal is at risk of having but does not have Helicobacter infection or has a Helicobacter infection. The attenuated Salmonella vector further comprises an htrA or nirB promoter. The vector and be used in inducing an immune response against Helicobacter in a mammal. The vector can be used to treat Helicobacter induced gastroducdenal diseases, including acute, chronic or atrophic gastric sarcinoma. Attenuated Salmonella vector pHUR3 was constructed expressing UreA and UreB and including an E. Coli AmpR gene. The present sequence represents a protein or peptide encoded by the pHUR3 or plasmid. NOTE: pHUR3 is represented by both ABB55112 and ABB5512 and ABB5512 and ABB5512 and ABB5513, yet Figure 4 shows all the peptides being expressed by the one sequence, therefore all encoded peptides are cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         483
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                                                                                                                                                                                                                                                                                                                                                                       76.1%; Score 2281; DB 4;
73.0%; Pred. No. 2.7e-190;
tive 76; Mismatches 77;
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Best Local Similarity
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AAR74337 standard; protein; 569

AAR74337

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Immunogenic composition against Helicobacter infection - also gene fragment(s) and protein(s) from Helicobacter urease gene cluster and heat shock protein(s).
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                                                                                 UreB; vaccine; Helicobacter infection; UreI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ^ Match 74.8%; Score 2244; DB 2; Local Similarity 72.5%; Pred. No. 4.7e-187; les 411; Conservative 71; Mismatches 85;
                                                                                                                                                                                                                                                                                  & RECH MEDICALE
                                                                                                                                                                                                                                                                                                              Ferrero R;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 10; Fig 3; 128pp; English.
                                                      Helicobacter felis urease UreB
                                                                                                                                                                                                              93WO-EP003259
                                                                                                                                                                                                                                         93WO-EP003259
             (revised)
(first entry)
                                                                                                                                                                                                                                                                                                              Labigne A, Suerbaum S,
                                                                                                                                                                                                                                                                    PASTEUR.
                                                                                                                                                                                                                                                                                                                                        WPI; 1995-200383/26
                                                                                                heat shock protein.
                                                                                                                          Helicobacter felis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 569 AA;
                                                                                 UreA;
                                                                                                                                                                                                                                                                    (INSP ) INST
(INRM ) INST
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02-NOV-1995
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482 541 481 IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT FEVFVDGKLCTSKPTSQVPLAQRYTFF 568 completed: November 28, 2005, 08:14:37 ne : 188.28 secs 422 482 Search co 8 6 8 ò В 셤 8

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Sequence 3, Appli
Sequence 15, Appli
Sequence 6, Appli
Sequence 9, Appli
Sequence 5, Appli
Sequence 252, Appli
Sequence 252, Appli
Sequence 8611, A
Sequence 8611, A
Sequence 40, Appli
Sequence 39, Appli
Sequence 20, Appli
Sequence 39, Appli
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Sequence 2, Appli
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                                                                                                  November 28, 2005, 08:11:38; Search time 160.242 Seconds (without alignments) 1481.056 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MKMKKQEYVNTYGPTKGDKV......KLCTSKPTSQVPLAQRYTFF
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(cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*

cqn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USO9_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USO3_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*

cgn2_6/ptodata/1/pubpaa/USIOB_PUBCOMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Sequence 70574, A Sequence 6526, Ap Sequence 78027, A Sequence 7, Appli Sequence 11, Appli Sequence 12, Appli Sequence 12, Appli Sequence 2, Appli Sequence 51072, A Sequence 51072, A Sequence 64615, A Sequence 64617, A Sequence 64617, A Sequence 64615, A Sequence 64617, A Sequence 64610, Appli Sequence 8610, Appli Sequence		Length 568; Indels 0; Gaps 0; ELKFGAGKTIREGAGGSNSP 60	3VSPHMVVGVGTEAL 120 3VSPHMVVGVGTEAL 120 TNATTITPGKWNLHR 180 TNATTITPGKWNLHR 180	TPSAIDHCLSVADEY 240   TPSAIDHCLSVADEY 240   TPSAIDHCLSVADEY 240   TTWAGELNILPSSTT 300   TTWAGELNILPSST 300   TTWAGEL
US-10-282-122A-70574 US-10-724-972A-6526 US-10-282-122A-44443 US-10-282-122A-78027 US-10-621-833-7 US-10-731-877-1 US-10-731-877-1 US-10-731-877-1 US-10-731-877-1 US-10-731-877-1 US-10-731-877-1 US-10-731-877-1 US-10-731-14057 US-10-282-122A-64617 US-10-282-122A-64617 US-10-282-122A-64617 US-10-156-761-14635 US-10-282-122A-64617 US-10-156-761-1635 US-10-16-761-1635 US-10-186-761-10252 US-10-335-977-8610	ALIGNMENTS 994B 25Alel N.V. r vaccine es 63 3/904,994B	Score 2999; DB 3; Pred. No. 1.4e-258; ; Mismatches 0; RLGDTDLWAEVEHDYTTYGE	DENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVGVGTEAL	MLRAABEYSMNVGFLGKGNSSSKKQLVEQVEACAIGFKLHEDWGTTPSAIDHCLSVADEY MLRAABEYSMNVGFLGKGNSSSKKQLVEQVEACAIGFKLHEDWGTTPSAIDHCLSVADEY MLRAABEYSMNVGFLGKGNSSSKKQLVEQVEACAIGFKLHEDWGTTPSAIDHCLSVADEY DVQVCIHTDTVNREAGYDDTLNAANGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTT
7.6.6 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	SULT 1 1:09-904-994B-3 CAPA-994B-3 EQUENCE 3, Application US/09904994B PUBLICATION NO. US20040005325A1 GENERAL INFORMATION US TITLE OF INVENTION: Helicobacter variants REFERENCE: Degoedesequenties CURRENT APLICATION NUMBER: US/09/9 CURRENT FILING DATE: 2001-07-13 NUMBER OF SEQ ID NOS: 21 SEQ ID NO 3 LENGTH: 568 TYPE: PRF TYP	100.0%; larity 100.0%; Conservative 0 KKOEYUNIYGPIKGDKV	DENTLDLVITNAMILDYTGI 	EYSMNYGFLGKGNS EYSMNYGFLGKGNS HTDTVNEAGYVDDT HTDTVNEAGYVDDT HTDTVNEAGYVDDT INTVAEHLDMLMTC
1789.5 1788.5 1784.5 1779.5 1779.5 1779.5 1753.5 1753.5 1753.5 1769.5 1699.5 1691.5 16	SULT 1  -09-904-994B-3  Sequence 3, Application U  Publication No. US2004000  GENERAL INFORMATION:  TPLIC OF INVENTION: Hell  FILE REFERENCE: Degoede  FURRENT APPLICATION: Hell  FURRENT FILING DAFE: 2  NUMBER OF SEQ ID NOS: 21  SOFTWARE: PATENTIN Ver.  SEQ ID NO 3  LENGTH: 568  LENGTH: 568  TYPE: PRT  ORGANISM: Helicobacter  -09-904-994B-3	Query Match Best Local Similar: Matches 568; Com    MKWKKQ)	61 DENTLD               61 DENTLD 121 AGEGMI 121 AGEGMI 121 AGEGMI	
0 0 0 1 0 1 0 0 0 0 0 0 1 0 1 0 0 0 0 0	RESULT 1 US-09-904 S-09-904 S-09-904 GENERAL PILE R PILE R CURREN CURREN NUMBER SOFTWAL SEO ID IENGT TYPE: TYPE: TYPE: CORGAN	Query Best Matcl Qy Db	& & & & &	8 4 8 4 8 4

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                                                                                               Sequence 6, Application US/09904994B
Publication No. US20040005325A1
GENERAL INFORMATION:
APPLICANT: AKZO No. US20040005325A1e1 N.V.
TITLE OF INVENTION: Helicobacter vaccine
FILE REFERENCE: Degoedesequenties
CURRENT APPLICATION NUMBER: US/09/904,994B
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver. 2.1
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Publication No. US20040005325A1
GENERAL INFORMATION:
APPLICANT: AKZO No. US20040005325A1e1 N.V.
TITLE OF INVENTION: Helicobacter vaccine
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                                                                                    HGKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPK
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                        421 YIGSVEECKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPOPVYYREMFGH
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Pred. No. 2.9e-256;
4; Mismatches 2;
                                                                                                                                                                                                                                                                                                               Sequence 15, Application US/09904994B
Publication No. US20040005325A1
GENERAL INFORMATION:
TITLE OF INVENTION: Helicobacter vaccine
FILE REFERRNCE: Degoedsequenties
CURRENT APPLICATION NUMBER: US/09/904,994B
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin Ver: 2.1
SOFTWARE: 568
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ORGANISM: Helicobacter felis
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Best Local Similarity 98.9
Matches 562; Conservative
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                                                                                                                                                            Length 568;
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                                                                                                                                                        Score 2953; DB 3;
Pred. No. 1.8e-254;
5; Mismatches 5;
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Publication No. US20040005325A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Helicobacter vaccine
FILE REFERENCE: Degoedesequenties
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 21
SQOFTWARE: Patentin Ver. 2.1
SQOFTWARE: Patentin Ver. 2.1
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FILE REFERENCE: Degoedesequenties
CURRENT APPLICATION NUMBER: US/09/904,994B
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 21
SEQTYARE: Patentin Ver. 2.1
SEQ ID NO 12
LENGTH: 568
                                                                                                                                                           98.5%;
98.2%;
                                                                                                   TYPE: PRT
; ORGANISM: Helicobacter felis
US-09-904-994B-12
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CRGANISM: Helicobacter felis

US-09-904-994B-9
                                                                                                                                                         Query Match
Best Local Similarity 98.2<sup>1</sup>
Matches 558; Conservative
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US-09-904-994B-9
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Publication No. US20040142343A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Zhu, Jiaqian
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
TITLE OF INVENTION IN DIAGNOSTIC AND TREATMENT METHODS
CURRENT APPLICATION NUMBER: US/10/639,273
CURRENT FILING DATE: 2002-08-12
PRIOR FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PTI PYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSS
                                                                                      1 MKMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSP
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Score 2588; DB 3; Length 496;
Pred. No. 5.8e-222;
1; Mismatches 2; Indels
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US-10-639-273-5
86.3%;
99.4%;
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SEQ ID NO 5
LENGTH: 569
    Query Match
Best Local Similarity 99.4*
Matches 489; Conservative
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                                                               LRAAEEYSMINGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
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    121
                                                                                  GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
                                                                                                          AEGLIVTAGGIDTHIHFISPQOIPTAFASGITTMIGGGTGPADGTNATTITPGRWNLKTM 182
                                                                                                                                                                   LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD 241
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APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANTON: IN DIAGNOSTIC AND TREATMENT METHODS
FILE REFERENCE: 19603/381
CURRENT APPLICATION NUMBER: US/10/639,273
PRIOR APPLICATION NUMBER: 60/404,337
PRIOR FILING DATE: 2002-08-16
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                         SHELDLVLTNALIVDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVCNNLCVGPATEALA
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  62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA
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ilarity 73.7%; Pred. No. 5.3e-196;
Conservative 74; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *:| |||| ||| || || XKVKVDGKEVTSKAADKISLAQLYNLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/10639273
Publication No. US20040142343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Helicobacter heilmannii
US-10-639-273-38
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SEQ ID NO 38
LENGTH: 568
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Best Local &
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APPLICANT: Al-Garawi, Amal APPLICANT: Miler, Charles APPLICANT: Miler, Charles APPLICANT: Tomb, Jean Francois APPLICANT: Oomen, Raymond P. TITLE OF INVENTION: Identification of Polymucleotides TITLE OF INVENTION: Encoding No. US20020160456Alel Helicobacter Polypeptides in the TITLE OF INVENTION: Genome TITLE OF INVENTION: Genome TITLE OF INVENTION: Genome CURRENT APPLICATION NUMBER: US/09/895,913A CURRENT FILING DATE: 2001-06-29 PRIOR FILING DATE: 2001-06-29 PRIOR FILING DATE: 197-06-24 NUMBER OF SEQ ID NOS: 368
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GEGLIVTAGGIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRRNLKWM 182
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Publication No. US20040052799A1
GENERAL INFORMATION:
APPLICANT: DOUGLAS SMITH et al
APPLICANT: DOUGLAS SMITH et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO HELICOBACTER PYLORI FOR
DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                              Length 569;
                                                                                                                                                                                                               Indels
                                                                                                                                                                76.6%; Score 2297; DB 4; 73.4%; Pred. No. 7.2e-196;
                                                                                                                                                                                                               76; Mismatches
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ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: Windows NT 4.0
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543 YHVFVDGKEVTSKPANKVSLAQLFSIF
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CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKF
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
SOFTWARE: PatentIn version 3.1
SEQ ID NO 58611
LENGTH: 569
                                                                                           ORGANISM: Helicobacter pylori
                                                                                                                                                              Query Match
Best Local Similarity 73.44
Matches 416; Conservative
                                                                                                                    US-10-282-122A-58611
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APPLICANT: Xu, H.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/201, 30
FRIOR APPLICATION NUMBER: 60/201, 32
FRIOR APPLICATION NUMBER: 60/201, 727
FRIOR APPLICATION NUMBER: 60/201, 33
FRIOR APPLICATION NUMBER: 60/230, 335
FRIOR APPLICATION NUMBER: 60/242, 578
FRIOR APPLICATION NUMBER: 60/242, 578
FRIOR APPLICATION NUMBER: 60/242, 578
FRIOR FILING DATE: 2000-10-23
FRIOR FILING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/253, 625
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-06
FRIOR APPLICATION NUMBER: 60/267, 636
FRIOR FILING DATE: 2001-02-06
FRIOR FILING FILING DATE: 2001-02-06
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                                                                                                                      VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
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Yamamoto, Robert
Forsyth, R.
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US-10-282-122A-58611
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APPLICANT:
APPLICANT:
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Sequence 40, Application US/10639273

Publication No. US200401423431

Publication No. US200401423431

Sequence 40, Application No. US200401423431

APPLICANT NORMATION:

APPLICANT: Simpson, Kenneth W

FILE REFERENCE: 19603/3881

CURRENT ELLO OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS

FILE REFERENCE: 19603/3881

CURRENT FILING DATE: 2003-08-12

PRIOR FILING DATE: 2003-08-12

PRIOR FILING DATE: 2002-08-16

NUMBER OF SEQ ID NOS: 41

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 40

TYPE: PRI

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RESULT 11
US-10-639-273-40
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   CURRENT APPLICATION DAIRS:
APPLICATION NUMBER: US/10/335,977
FILING DATE: 30-Dec-2002
PRIOR APPLICATION DATE:
APPLICATION DATE: 08/993,002
FILING DATE: 17-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: MAME: MAMER: 36,207
REFERENCE/DOCKET NUMBER: 36,207
REFERENCE/DOCKET NUMBER: GTN-018
TELEPHONE: (617)727-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature; LOCATION: (B) LOCATION 1...569; SEQUENCE DESCRIPTION: SEQ ID NO: 8611: US-10-335-977-8611
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Helicobacter pylori
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HYPOTHETICAL: YES
ORIGINAL SOURCE:
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; Sequence 39, Application US/10639273
; Publication No. US20040142343A1
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                                                                                                                                                                                                                                                                                                  Gaps
        APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Simpson, Kenneth W
APPLICANT: Zhu, Jiaqian
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR UTITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR UTITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
TILE REPERENCE: 1960/33881
CURRENT PELLING DATE: 2003-08-12
PRIOR PPLING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PATENTIN VET: 2.1
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                                                                                                                                                                                                                                                                      Length 569;
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                                                                                                                                                                                                                                                                    74.8%; Score 2244; DB 4; 72.5%; Pred. No. 3.9e-191; tive 71; Mismatches 85;
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Patent No. US20010019834A1
GENERAL INFORMATION:
APPLICANT: Daewoong Pharmaceutical Co,
APPLICANT: Kim, Byung-O
APPLICANT: Shin, Sung-Seup
APPLICANT: Yu, Young-Hyo
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ORGANISM: Helicobacter felis
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.54
Matches 411; Conservative
GENERAL INFORMATION:
                                                                                                                                                                                                                                        US-10-639-273-39
                                                                                                                                                                                SEQ ID NO 39
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APPLICANT: Jung, Hyung-Jin

TITLE OF INVENTION: Recombinant Microorganisms Expresing Antigenic Proteins of Heliob
FILE REFERENCE: 0136/06140
CURRENT APPLICATION NUMBER: US/09/402,100
CURRENT FILING DATE: 1999-09-27
EARLIER APPLICATION NUMBER: KR 97-11950
BARLIER PILING DATE: 1997-03-31
EARLIER FILING DATE: 1997-03-31
EARLIER FILING DATE: 1997-03-31
NUMBER OF SEQ ID NOS: 48
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: UreB/CTXA2B Chimeric protein
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Sequence 41, Application US/10639273
Publication No. US20040142343A1
GENERAL INFORMATION:
APPLICANT: Chang, Yung-Fu
APPLICANT: Simpson, Kenneth W
                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
Park, Myung-Hwan
Choi, Deok-Joon
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APPLICANT: Xu, A.

APPLICANT: Xu, A.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/101,078

PRIOR PELING DATE: 2000-03-21

PRIOR PELING DATE: 2000-03-23

PRIOR PLLING DATE: 2000-05-23

PRIOR PLLING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PLLING DATE: 2000-05-06

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR PLLING DATE: 2000-09-06

PRIOR PLLING DATE: 2000-09-06

PRIOR PLLING DATE: 2000-10-23

PRIOR PLLING DATE: 2000-11-27

PRIOR PLLING DATE: 2000-12-26

PRIOR PLLING DATE: 2001-02-09

PRIOR PLLING DATE: 2001-02-09

PRIOR PLLING DATE: 2001-02-09

PRIOR PLLING DATE: 2001-02-06

PRIOR PLLING DATE: 2001-02-16

PLLING DATE: 2001-02-16

PLLING DATE: 2001-02-16

PRIOR PLLING DATE: 2001-02-17

PRIOR PLLING DATE: 2001
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                               Carr, Grant
Yamamoto, Robert
Forsyth, R.
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APPLICANT: Zhu, Jiaqian
TITLE OF INVENTION: HELICOBACTER BIZZOZERONII UREASE GENES AND THEIR USES
TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
TITLE OF INVENTION: IN DIAGNOSTIC AND TREATMENT METHODS
FILE REPERRNCE: 19603/3881
CURRENT APPLICATION NUMBER: US/10/639,273
CURRENT APPLICATION NUMBER: 00/404,337
PRIOR PILING DATE: 2003-08-16
NUMBER OF SEQ ID NOS: 41
SOFTWARE: 2002-08-16
SEQ ID NO 41
LENGTH: 569
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                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Helicobacter hepaticus
US-10-639-273-41
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US-10-282-122A-47638
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                                                                        1 MKMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSP
                                        Gaps
                                       2
Query Match 64.1%; Score 1922; DB 4; Length 5 Best Local Similarity 61.3%; Pred. No. 2.3e-162; Matches 348; Conservative 97; Mismatches 121; Indels
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Sequence 47638, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mang, Liangsu
APPLICANT: Aamudio, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari
APPLICANT: Oyleen, Kari
APPLICANT: Oyleen, Kari
APPLICANT: Wall, Daniel

Search completed: November 28, 2005, 08:24:32 Job time : 162.242 secs

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JS-10-793-626-118
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67, Appl
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                                                                                                              November 28, 2005, 08:14:48; Search time 7.15365 Seconds (without alignments) 240.659 Million cell updates/sec
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1 MKWKKQEYVNTYGPTKGDKV......KLCTSKPTSQVPLAQRYTFF 568
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5: /cgn2_6/ptodata/1/pubpaa/US09 NEW PUB.pep:*
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26 84 2.8 444 7 US-II-074-I76-I70 Sequence 170, App 27 84 2.8 447 1 US-II-075-I70-81 Sequence 170, App 28 83.5 2.8 447 1 US-II-0-858-730-219 Sequence 219, App 30 83.5 2.8 426 1 US-II-0-858-730-81 Sequence 166, App 31 82.5 2.8 547 1 US-II-0-81-246 Sequence 166, App 31 82.5 2.8 547 1 US-II-075-194-12 Sequence 12, App 32 82 2.7 735 1 US-II-184-380-80 Sequence 12, App 134 81.5 2.7 426 1 US-II-184-380-80 Sequence 1082, App 34 81.5 2.7 426 1 US-II-0828-730-80 Sequence 1082, App 37 80.5 2.7 341 US-II-074-I76-4 Sequence 309, App 38 80.5 2.7 341 US-II-074-I76-4 Sequence 218, App 139 80.5 2.7 341 US-II-074-I76-4 Sequence 218, App 140 79:5 2.7 1432 1 US-II-073-626-342 Sequence 218, App 141 79:5 2.7 152 1 US-II-0793-626-296 Sequence 218, App 141 79:5 2.7 152 1 US-II-0793-626-296 Sequence 222, App 44 78:5 2.6 1201 1 US-II-074-I76-256 Sequence 222, App 44 78:5 2.6 1201 1 US-II-074-176-256 Sequence 226, App 44 78:5 2.6 1201 1 US-II-074-176-256 Sequence 226, App 44 78:5 2.6 1201 1 US-II-074-176-246 Sequence 226, App 54 78:5 2.6 1201 1 US-II-074-I76-246 Sequence 226, App 55 2.7 154 1 US-III-074-I76-256 Sequence 226, App 56 226 226 226 Sequence 226, App 57 226 1201 US-II-074-I76-256 Sequence 226, App 57 226 1201 US-II-074-I76-256 Sequence 226, App 58 70:5 2.6 1201 US-II-074-I76-246 Sequence 226, App 58 70:5 2.6 1201 US-II-074-I76-344 Sequence 236, App 58 70:5 2.6 1201 US-II-074-I76-344 Sequence 2344, App 58 70:5 2.6 1201 US-II-074-I76-344 Sequence 2344, App 58 70:5 2.6 1201 US-II-074-I76-344 Sequence 344, App 58 70:5 2.6 1201 US-II-074-I76-344 Sequence 344, App
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## ALIGNMENTS

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TTPTIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMT 358
GENERAL INFORMATION:
APPLICATION NO. US20050255478A1
GENERAL INFORMATION:
APPLICANT: KIMMERELY, WILLIAM JOHN
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PU3480US
CURRENT PILING DATE: 2004-03-04
RELOR APPLICATION NUMBER: 60/164,258
PRIOR FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 118
LENGTH: 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQS---N
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US-10-793-626-118
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                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 58.2%
Matches 332; Conservative
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124 VKEVKAVÝPNATÝKPDSVKGKDÝTĽAADAIYPQMDKSAPFIGADQAWKSGÝT---GKG-- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 DIG-----IKNGKIHGI------GKAGNKDMQDGVSPHMVVGVGTEALAGEG 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----KQLVEQVEAGAIGFKLH 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------LGQADDFSGKDVKGKVAVIQRGVIPFVDKAENAKNAGAIGAVIYNNA 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         331 LQFSQSR-----IRPG----SIAAEDVLHD-----MGVIAMISSDSQAMGRAGE 370
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                   1 MKMKKQEYVN-TYGP--TKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 4.1%; Score 123.5; DB 1; Best Local Similarity 20.3%; Pred. No. 0.015; Matches 141; Conservative 85; Mismatches 231;
                                                                                                                                                                                                                                                                                  APPLICANT: Clausen, ib Groth
APPLICANT: Jorgensen, Steen Troels
APPLICANT: Jorgensen, Steen Troels
APPLICANT: OBSEN, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cel
FILE REFERENCE: 10294.204-US
CURRENT APPLICATION WUMBER: US/10/510,386
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175 KWNLHRMLRAAEEYSMNVGFLGKGNSSSK----
                                                                                                                                                                                                             ; Sequence 2, Application US/10510386; Publication No. US20050244922A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Bacillus licheniformis US-10-510-386-2
                                                                                                                                                                                                                                                                    APPLICANT: Andersen, Jens Tonne APPLICANT: Clausen, Ib Groth
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                                                                              SEYIGSVEEG 428
                                                                                                                 SEYVGSIEPG 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            119 ALAGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYDVQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSS 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTPTIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMT 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNPTLPYTHNTVDEHLDMVMITHHINAAIPEDIAFADSRIRKETIAAEDVLQDMGVFSMI 361
421
                                                                                                                                     SEYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMF 478
                                                                                                                                                          GHHGKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVD 538
                                                                                                                                                                                                                                   64 RDDVNVADLVISNAVIIDYDKVVKADIGIKNGYIFAIGNAGNPDIMDNVD--IIIGSTTD 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 HRMLEAAEGL PINVGFTGKGQATNPTALIEQINAGAIGLKVHEDWGATPSALSHALDVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQS----N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSDSQAMGRVGEVVTRTWQVAHRMKEQRGPLDGDFEYHDNNRIKRYIAKYTINPAITHGI
                                                          SSDSQAMGRAGEVI PRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 1380.5; DB 1; Length
; Pred. No. 1.3e-102;
68; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Biosynexus Incorporated
APPLICANT: Boster, Simon
APPLICANT: Goster, Simon
APPLICANT: Mond, James
TITLE OF INVENTION: Antigenic Polypeptides
FILE REFERENCE: PROGESHOOF CURRENT PLING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: US 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: GB 0118825.9
PRIOR FILING DATE: 2001-08-02
PRIOR PRILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 424
SEQ ID NO 182
                                                                                                                                                                                                                                                                                        PKTFEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                           Sequence 182, Application US/10485517
Publication No. US20050256299A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Staphylococcus aureus
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59.3%;
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Matches 255; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                       ----SITFVS---KVAYENGVKEKLGLERQVLPV 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 K-DSGLDVNRGIVVNDYMQTSDSHIYAVGECAEHDGKVYGLVAPLYEQGKVLADYLTGKE 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEALAGEGM------IITAGGI--DSHTH---------FLSPQQFPTALA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 YGDTD------DGSRF------YNWMKKHETLEDYTL-VSLLHKGDEDAGTSIADM 410
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 IHAYHIEGAGGGHSP-----DVITMAGELNILPSSTT-------PTIPY 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               404 YISKYTINPAL------THGVSEYIGSVEEGKIADLVVWNPAFFGVKPKIV 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         411 SDDETICGCNGVDKGTIVNAITSKGLTSVDE----VTKATKAGNSCGKCKGQIGELLQYT 466
                                                                                                                                                                                                                                                          Sequence 90. Application US/10793626
Publication No. US20050255478A1
GENERAL INFORMATION
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: PUJ480US
CURRENT APPLICATION NUMBER: US/10/793,626
CURRENT APPLICATION NUMBER: G0/164,258
PRIOR APPLICATION NUMBER: 60/164,258
PRIOR PLING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 IGDKDV------EAIKLADGRVIE------TDLVVMAVGIRPYTEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     527 YLNMVYPFEHRD-----EKDSRFANERYHANİQNDGTFSVIPQMRGGVTDADQLIRLGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              306 TINTV--AEHLDMLMTCHHLDKR-----IREDLQFSQSRIRPGSIAAEDVLHDMGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 355 IA-----MTSSDSQAMGRAG---EVIPRTWQTAD-KNKKEFGKLPEDGKDNDNFRIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22 LGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPDENTLDLVITNAMIIDYTGIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTHER INFORMATION: Description of Artificial Sequence: synthetic;
CTHER INFORMATION: amino acid sequence
US-10-793-626-90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
3.5%; Score 105.5; DB 1; Length 801;
Best Local Similarity 19.5%; Pred. No. 0.39;
Matches 128; Conservative 75; Mismatches 244; Indels 211;
                                                                                                                                                                  1273
                                                                   1139 DQTKGLTTPKLTVGNNNGKGIVIDSKDGQNTITGLSNTLANVT--
                                                                                                                                                   516 KNCRNITKKDFKFND--KTAK----ITVDPKTFEVFVDGKL
                                          GKAKFDT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                 RESULT 5
US-10-793-626-90
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LENGTH: 801
                                              482
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Sequence 11, Application US/11013759
Publication No. US20050249747A1
GENERAL INFORMATION:
APPLICANT: Loosmore, Sheena M.
APPLICANT: Saaaki, Ken
APPLICANT: Yang, Yan Ping
APPLICANT: NECHEL H.
ITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
ITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REFERENCE: 1038-921MS:1jb
CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT FILING DATE: 2004-12-16
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOSTWARE PATENTING US: 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 AGAIGFKLHE-DWGTTPSAIDHCLSVADEYDVQVCIHTDTVNEAGYVDDTLNAMNGRAIH 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          271 AYHIEGAGGGHSPDVITMAGELNILPSSTTPTIPYIIPYTINTVAEHLDMLMTCHHLDKRIRED 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          331 LQFSQSRIRPGSIAAEDVLHDMGVIAMTSSDSQAMGRAGEV-----IPRTWQTADKNK 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384 KEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEYIGSVEEGKIADLVVWNPAFFGV 443
                                              ----ERQVLPVKNC 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPDENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGN-----KDMQDGVSP--- 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --HMVVGVGTEAL-----AGEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                875 EIHTTKGTADTÄLQTFKVKKDGÄTDDETITVG-------KDGTQNGKTV--- 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 GTGPVDGTNATTITPGK-----WNLHRMLRAAEEYSMNVGFLGKGNSSSKKQLVEQVE 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----KPKIVIKG----GMVVFSEMGDSN-----ASVPTPQPVYYREMFGH---H 481
      602 SYGTFL--KDKGKQTKKQAFTIENLSSHRKAY---QLEYSFKGTGITVS--GTERVVVPA 654
                                                                                      655 NQT------GKAAAKVTV-----NSAKTKAGTYEGTVYIREDGRKVAEIPLL 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 YVNTY-----GPTKGDKVRLGDTDLWAEVEHDYTTYGE--ELKFGAGKTIREGMGQSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.8%; Score 113; DB 7; Length 2314;
20.0%; Pred. No. 0.47;
iive 68; Mismatches 201; Indels 244; Gaps
                                                469 PQPVYYREMFGHHGKAKFDTSITFVSKVAYENGVKEKLGL---
                                                                                                                                                       519 RNITKKDFKFNDKTAKITVDP----KTFEVFVDG 548
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Best Local Similarity 20.09
Matches 128; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 11
LENGTH: 2314
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LENGTH: 1992
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                                                                                                             LENGTH: 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 FSEMGDSNASVPTPQPVY-----YREMFGHH-GKAKFDTSITFVSKVAYENGVKEKL 506
 ----YYREMFGHHGKAKFDTSIT 491
                        PIIKYII----EHGGKAILLSHLG-RVKSDADKKELSLKPVAERLSELL-DKPVTFVPSN 95
                                                                                            |: : : | |: |
|-----KELYLRIMEAKKAVENEPWETIVENK 790
                                                                     FVSKVAYENGVKEKLGLEROVLPVKNCRNITKKDFKFNDKTAKITVDPKTFEVFVDGK 549
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Sequence 186, Application US/11074176

GENERAL INFORMATION:
APPLICANT: Russell, William M.
APPLICANT: Alternanner, Todd R.
APPLICANT: Alternann, Eric
APPLICANT: Manu, Eric
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
                                                                                                                                                                                                                                                                                       APPLICANT: ALECTMAIN, ETIC
APPLICANT: MCAULIffe, Olivia
APPLICANT: MCAULIffe, Olivia
APPLICANT: Peril, Andrea Azcarate
APPLICANT: Peril, Andrea Azcarate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Therefore
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074,176
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; DB 7; Length 403; 0.39;
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 -----SEMGDSNASVPTPQPV
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 354
                                                                                                         745 WLERMGFENVKNVLLNQEKO----
                                                                                                                                                                                              Sequence 354, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Lactobacillus acidophilus
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Matches 72; Conservative
 I KGGMVVF-
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US-11-074-176-186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 FSEMGDSNASVPTPQPVY-----YREMFGHH-GKAKFDTSITFVSKVAYENGVKEKL 506
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APPLICANT: Yang, Yan Ping
APPLICANT: Yang, Yan Ping
APPLICANT: Ktein, Michel H
TITLE OF INVENTION: RECOMBINANT HICH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REPERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,759
CURRENT FILING DATE: 2004-112-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR PILING DATE: 1999-07-27
SOFTWARE: PALENTING DATE: 2004-12-16
SEQ ID NOS: 32
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NOS: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 DSQAMGRA-----GEVI---PRTWQTADKN--KKEFGKLPEDGK------DNDNFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             301 PTIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSS
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                                                                                                                                                                                                                                                                                                                                                            DB 7; Length 408
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                      Query Match 3.3%; Score 100; DB 7; L. Best Local Similarity 24.6%; Pred. No. 0.4; Matches 72; Conservative 43; Mismatches 112;
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Best Local Similarity 21.8%; Pred. No. 4.4;
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: 60/551,161
PRIOR FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 186
                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Lactobacillus acidophilus
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Publication No. US20050249747A1
GENERAL INFORMATION:
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ORGANISM: Moraxella catarrhalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Loosmore, Sheena M.
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09   273   HIEGAGGGHSPDVITMAGELNILPSSTTPTIPYTIN-TVAEHLDML 317	RESULT 10  US-11-013-759-4  i Sequence 4, Application US/11013759  i Publication No. US20050249747A1  i GENERAL INFORMATION:  i APPLICANT: LOGENCE, Sheena M.  APPLICANT: Sasaki, Ken  APPLICANT: Yang, Yan Ping  i APPLICANT: NECHEL H.  ITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  ITLE OF INVENTION: PROTEIN OF MORAXELLA  ITLE OF INVENTION: PROTEIN OF MORAXELLA  ITLING DATE: 1038-921MIS:jb  CURRENT APPLICATION NUMBER: US/11/013,759  CURRENT FILING DATE: 1999-07-27  NUMBER OF SEQ ID NOS: 32  SOFTWARE: PATCH OF NOS: 32  SOFTWARE: PA	Query Match         3.3%; Score 99.5; DB 7; Length 2047;           Best Local Similarity 21.8%; Pred. No. 4.6;           Matches 114; Conservative 49; Mismatches 160; Indels 201; Gaps 30;           QY 54 MGQSNSPDE-NTLDLVITNAMIIDYTGIYKADIGIKNGKI-HGIGKAGNKDMQDG 106           Db 976 VGQKNANNQVNTLTLKGENGLNIKTDKNGTVTFGINTTSGLKAGKSTLNDG 1026	0.7   USPHMVGVGTEALAGEGMI-ITAGGIDSHTHFLSPQQFPTALANGVTTWFGGGTGPVDG 165	Qy 213 GAIGFKLHEDWGTTPSAIDHCLSVADEYDVQVCIHTDTVNEAGYVDDTLNAMNGRAIHAY 272
009 T-TRITTPGKWNLHRWLRAAEEYSMNVGFLGKGNSSSKK	438 PAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHHGK  1212VLSAGFNLQGNGEAVDFVSTYDTVNFADGNATT  493 VSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKIT 536	PRIOR FILING DATE: 1999-07-27 NUMBER OF SEQ ID NOS: 32 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 13 LENGTH: 1992 TYPE: PRI ORGANISM: Moraxella catarrhalis	Query Match         3.3%;         Score 99.5;         DB 7;         Length 1992;           Best Local Similarity 21.8%;         Pred. No. 4.4;         No. 4.4; <t< td=""><td>  107 VSPHMVVGVGTEALAGEGMI-ITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDG 165                                      </td></t<>	107 VSPHMVVGVGTEALAGEGMI-ITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDG 165

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114 ILIHLKNFATRPYTIHPHGVFYEKÖ---SEGSLYPDGSSGPLKADDSVPP----- 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330016128
CURRENT APPLICATION NUMBER: US/10/131,826A
CURRENT PILING DATE: 2002-04-24
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18.1%; Pred. No. 3.8;
ative 81; Mismatches 162; Indels 206;
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493 VSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKIT
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PRIOR APPLICATION NUMBER: 60/059184
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FLING DATE: 1997-09-19
PRIOR FLING DATE: 1997-09-19
                                                                                                                                                                      Sequence 234, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-18
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059113
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PRIOR APPLICATION NUMBER: 60/059115
PRIOR FILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/059122
PRIOR APPLICATION NUMBER: 60/059122
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Gerritsen, Mary E.
Goddard, Audrey
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Wood, William
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Gurney, Austin L.
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Best Local Similarity 18.1
Matches 99; Conservative
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                                              1311 -SKVVYDVNVDD
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                                                                                                                                             ------VLSAG---FNLQGNGEAVDFVSTYDTVNFAD--GNATTAKVTYDDTSKT- 1310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1064 T--TRITRDE-------GFTGTNGSLDKSKPHLSKDGINAGGKKITNIQS 1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              166 TNATTITPGKWNLHRMLRAAEEYSMNVGFLGKGNSSSKK-------QLVEQVBA 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              273 HIEGAGGGH------SPDVITMAGELNILPSSTTPTIPYTIN-TVAEHLDML 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 MTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSDSQAMGRAGEVIPRTWQ 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            378 TADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEYIGSVEEGKIADLVVWN 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sacaki, Kennara APPLICANT: Sacaki, Kennara APPLICANT: Sacaki, Kennara APPLICANT: Yang, Yan Ping
APPLICANT: Yang, Yan Ping
APPLICANT: Klain, Michel High
APPLICANT: Klain, Michel High
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTBIN OF MORAXELLA
FILE REFERENCE: 1038-921MAS: 1)
CURRENT APPLICATION NUMBER: US/09/361,619
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 3.2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 7.2
378 TADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEYIGSVEEGKIADLVVWN 437
                                                                                              438 PAFFGVKPKIVIKGGMVVFSEMGDSNA--SVPTPQPVYYREMFGHHGKAKF---DTSITF 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3.3%; Score 99.5; DB 7; Length 2047;
21.8%; Pred. No. 4.6;
tive 49; Mismatches 160; Indels 201;
                                                                                                                                                                                                                                            ----Trievkokkugvkittur 1339
                                                                                                                                                                                                493 VSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKIT 536
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 7, Application US/11013759
Publication No. US20050249747A1
GENERAL INFORMATION:
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US-11-013-759-7
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Loosmore, Sheena M.
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                                                                                                                                                                                                                                              1311 -SKVVYDVNVDD-
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Gaps

Db 358 DKIKKFLTESHDRQAKGKAITKKKYIGIRMMSLTSSKAKELKDRHR 403  Qy 222 DWGTTPSAIDHCLSVADEYDVQVCIHTDTVNBAGYVDDTLNAMNGRAIHAYHIEGAGG 279	RESULT 14 US-11-013-759-9  US-11-013-759-9  Sequence 9, Application US/11013759  Publication No. US20050249747A1  SEQUENCE Sheena M.  APPLICANT: Loosmore, Sheena M.  APPLICANT: Assaki, Kan  APPLICANT: Wang, Yan Ping  APPLICANT: Klein, Michel H.  ITILE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE  ITILE OF INVENTION: PROTEIN OF MORAKELLA  FILE REFERENCE: 1038-921MLS:jb  CURRENT APPLICATION NUMBER: US/11/013,759  CURRENT FILING DATE: 1999-07-27  NUMBER OF SEQ ID NOS: 32  SOFTWARE: PATENTIN Ver. 2.1  SEQ ID NO 9  LENGTH: 2053  ITVE: RR	3.1%; 19.0%; vative 85. GDTDLWAEVE ; CAPLL    : VAQLKLVEELA LKVKLAKELTG LKVKLAKELTG TNDSNSIATKG	Qy	Qy 336 SRIRPGSIAAEDVLHDMGVIAMTSSDSQAMGRAGEVIPRTWQTADXNKKEFGKLPEDGKD 395     : :
Db 161TWIND TIPEGHAPTDADPACLTWIN 188  Qy 179 HRMLRAABEDYSMN'GFLG	Qy         277 AGGGHSPDVITMAGELNILPSSTTPTIPYTINTVAEHLDML 317           Db         300 MGNEIDVHTAFFHGQMLTTRGHHTDVANIFPATFVTAEMVPWEPGTWL 347           Qy         318 MTCHHLDKRIREDLQ	US-10-821-234-1465 US-10-821-234-1465 Sequence 1465, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION: APPLICANT: Labat, Ivan APPLICANT: Adarmani, Susan APPLICANT: Tang, Y. Tom APPLICANT: Tang, Y. Tom APPLICANT: Tang, Y. Tom APPLICANT: APPLICATION NUMBER: US/10/821,234 CURRENT FILING DATE: 2004-04-07 FILE REFERENCE: 821A CURRENT RILING DATE: 2003-04-07 PRIOR PILING DATE: 2003-04-07 PRIOR FILING DATE: 2003-04-07 NUMBER: OF SEQ ID NOS: 1704 SOFTWARE: pt. SEQ_genes Version 1.0 SEQ ID NO 1465 LENGTH: 480 TYPE: PRI CREATH: 480 TYPE: PRI CREATH: 480 SEQ ID NO 465 LENGTH: 480 TYPE: PRI CREATH: ARBITICAL ARBIT	Ouery Match  3.2%; Score 94.5; DB 1; Length 480;  Best Local Similarity 19.6%; Pred. No. 1.4;  Matches 66; Conservative 48; Mismatches 95; Indels 127; Gaps 18;  Qy 50 IREGMGQSNSPENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQD 105  Db 201 VASGSGFIVSEDGLIVTNAHVVTNKHRVKVELKNGATYEAKIKDVDEKADI 251  Qy 106GVSPHMVGVGTEALAGEGMIITAGGIDSHTHFLSPQQPFTALANGVTT 154  Db 252 ALIKIDHQGKLPVLLIGRSSELRPGE-FVVAIGSPFSLQNTVTTGIV 297	Qy         155

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SEO VLDKTPPSAPKVNPVTNKST-AVKGKAEANAAIIVKSGKKTIGTGKADKKGAFFVKIKKQ 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | :: | | : | | : | | 3.46 KILRGKQVLGTGTAGKSGAFSVKIPAQKAGQVLHV----AASGHQAETSLRTVVEKAPK 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            801 NPSVKRITNKDTAVTGRTAAGYTIKVKNACKKVIAGGRADASVSVKVKINKQKEYAVLYV 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        458 EMGDSNASVPTPQPVYYREMFGHHGKAKFDTSITFVS-KVAYENGVKEKLG-----LERQ 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                147 ALANGVITMFGGGTGPVDGTNATIITPGKWNLHRMLRAAEEYSMNVGFLGKGNSSSKKQL 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       402 KRYISKYTINPALTHGVSEYIGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMV----VFS 457
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                                                                          805 LSPTLPSIASPSGRNIALGNTIEEKDKSNAASIDDVLNAGFN--LKNNGKDKDFVSTYDT 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 GKIHGIGKAGNKDMQDGVS---PHMVVGVGTEALAGEGMIITAGGIDSHTHFLSPQQFPT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                622 TDIPSLVPDGNVTYMSGTSMAAPHVA-----AAAGLLL-----SQNPSLKPKQIAS 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              668 LLT-----ETTADVAFEEQDNPNPDYDL 690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             292 LNILPSSTTPTIPYINTVAEH-LDMLMTCHHLDKRIREDLOFS------OSRIRPG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           342 SIAAEDVILHDMGVIAMTSSDSQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRI 401
747 GVNITTNRATGTVTFGIDQSNGLTTPKLTVGSDTNGN--RLVIEQVPSADGNSTKNIIKG 804
                                             -----GMVVFSEMGDSNASVPTPQPVYYREMFGHHGKAK-----FDT 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.1%; Score 93; DB 1; Length 1047;
Best Local Similarity 19.2%; Pred. No. 5.7;
Matches 109; Conservative 75; Mismatches 227; Indels 156; Gaps
                                                                                                                                                                                                                                                                                             Sequence 200, Application US/10510386
Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Clausen, Ib Groth
APPLICANT: Clausen, Ib Groth
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
TITLE OF INVENTION: Improved Bacillus Host Cell
FILE REFERENCE: 10294.204-US
FILE REFERENCE: 10294.204-US
CURRENT FILING DATE: 2004-10-04
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.3
SEQ ID NO 200
LENGTH: 1047
                                                                                                                                                                    863 VDFIDGNATTATVTYDEANQTSKVAYDVNVDEK 895
                                                                                                                                       489 -----SITF----VSKVAYENGVKEK 505
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; ORGANISM: Bacillus licheniformis
US-10-510-386-200
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November 28, 2005, 08:13:38; Search time 46.4987 Seconds (without alignments) 1009.915 Million cell updates/sec
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1 MKMKKQEYVNIYGPIKGDKV......KLCISKPISQVPLAQRYIFF 568
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/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
/cgn2_6/ptodata/1/iaa/H_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
/cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
5.1.6
Compugen Ltd.
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                     Copyright
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Sequence 26, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 21, Appli Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 26887, A 5, Appli 5, Appli 27, Appl Sequence 26, Sequence 12, Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-338-920B-12 US-09-338-920B-6 US-08-432-697-26 US-08-466-248-26 US-08-920-095-3 US-08-920-095-3 US-08-920-095-3 US-09-431-705-5 US-09-431-705-5 US-09-431-705-5 US-09-338-920B-10 US-09-338-920B-10 US-09-338-920B-10 US-09-338-920B-10 US-09-338-920B-10 US-09-338-920B-10 US-09-338-920B-10 US-09-338-920B-10 US-09-328-352-912-16 US-09-328-352-5912-16 US-08-667-6458-5 US-08-667-648-5 US-08-667-648-7 US-08-667-648-7 US-08-667-648-7 US-08-667-648-7 US-08-467-648-7 SUMMARIES Query Match Length DB 60. 2298.5 2297 Score Result

•••••	Sequence 10192, A Sequence 2, Appli
US-08-466-248-25 US-09-602-777A-14 US-09-602-777A-16 US-09-3138-9208-14 US-09-318-9208-14 US-09-49-016-10606 US-09-49-016-10606 US-09-49-016-11503 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-1815 US-09-702-705-705-1815 US-09-702-705-705-705-705-705-705-705-705-705-705	US-09-949-016-10192 US-10-009-782A-2
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1787.5 1708 1619 1166 189.5 173.5 173.5 171.5 171.5 171.5 171.5 171.5 171.5 171.5	159.5 159
8444467989999999999999999999999999999999	44 45

## ALIGNMENTS

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62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                    243 VQVAIHTDTLNBAGCVEDTLEAIAGRTIHTFHTEGAGGGAAPDVIKWAGEFNILPASTNP
                                                                                                                                                                                                                                                                                                                                                                                                                 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                DB 2; Length 568;
                                                          APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas William D., Jr.
APPLICANT: Thomas P.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 06132/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR PILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 568
                                                                                                                                                                                                                                                                                                                                                                                 74; Indels
                                                                                                                                                                                                                                                                                                                                              76.6%; Score 2298.5; DB 2, 73.7%; Pred. No. 7.7e-214; tive 74; Mismatches 74;
            Sequence 12, Application US/09338920B
Patent No. 6709851
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Helicobacter heilmannii
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.7%
Matches 418; Conservative
JS-09-338-920B-12
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APPLICANT: Labigne, Agnes
APPLICANT: Bauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCES: 44
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
423 VGSVEVGKVADLVLWSPAFFGVKPNMIIKGGFIALSOMGDANASIPTPOPVYYREMFAHH 482
                                                    2 KWKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
                                     482 GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   76.5%; Score 2294; DB 1; 73.4%; Pred. No. 2.1e-213; ive 76; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03495.0137-02000
                                                                                                                                542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
PILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
PILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                   Sequence 26, Application US/08467822 Patent No. 5843460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 034
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1300 I Street, N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 26
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3315
COMPUTER READABLE FORM:
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Matches 416; Conserv
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                                                                                                                                             541
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                                                                         481
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SQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY 421
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                                                                    IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
                                                                                        GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
                    SQAMGRVGEVITRTWQTADKNKKEFGRLPEEKGDNDNFRIKRYISKYTINPAITHGISEY
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APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
APPLICANT: Monath, Thomas D., Jr.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFREENCE: 06122/02302
CURRENT APPLICATION UNMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
PRIOR APPLICATION NUMBER: US 08/928,081
PRIOR PILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FASESEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 76.6%; Score 2297; DB 2; Best Local Similarity 73.4%; Pred. No. 1.1e-213; Matches 416; Conservative 76; Mismatches 75;
                                                                                                                                                                                                                                        FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                             ; Sequence 6, Application US/09338920B; Patent No. 6709851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Helicobacter pylori
                                                                                                                                                                                                                                                                                                                                                                                  ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              RESULT 2
US-09-338-920B-6
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362
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Sequence 26, Application US/08466248
; Patent No. 6258359
; GENERAL INFORMATION:
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: TOWNORTH SAID SEQUENCES ENCODING SAID
                                                                                                                                                                                                                                                                                                                                                                                               GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITFGKWNLHRM 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 GEGLIVTAGGIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTNATTITPGRRNLKWM 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP 301
                                                                                                                                                                                                                                                                                                                                                                             ENTLDLVITNAMI I DYTGI YKADI GI KNGKI HGI GKAGNKDMQDGVS PHMVVGVGTEALA
                                                                                                                                                                                                                                                                                                                         TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                        pred. No. 2.1e-213, 76; Mismatches 75,
                                                                                                                                                                                                                          76.5%; Score 2294; 73.4%; Pred. No. 2.
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543 YHVFVDGKEVTSKPANKVSLAQLFSIF
TELECOMMUNICATION INFORMATION TELEPHONE: (202) 408-4000
               TELEPHONE: (202) 408-400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISCICS:
LENGTH: 569 amino acids
                                                                                                                                                                                                                            Query Match 76.5
Best Local Similarity 73.4
Matches 416, Conservative
                                                                                                            TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
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US-08-432-697-26
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US-08-466-248-26
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APPLICANT: Labigne, Agnes
APPLICANT: Saverbaum, Sebastien
APPLICANT: Saverbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Frerero, Informacian Compositions adainst
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        542
                       121
                                        GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Parent PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEVFVDGKLCTSKPTSQVPLAQRYTFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 26, Application US/08432697
Patent No. 6248330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-08-432-697-26
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122 GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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                                            482 GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Cynthia K. Lee et al.
TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02110-2804

ZIP: 02110-2804

MEDIUM TYPER FORM:
MEDIUM TYPER FOODPOTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76.4%; Score 2290; DB 1; 73.6%; Pred. No. 5.1e-213; tive 75; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/431,041
FILING DATE: 28-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30.162
REFERENCE/DOCKET NUMBER: 06132/013001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                542 FEVFVDGKLCTSKPTSQVPLAQRYTFF 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/920,095
                                                                                                                                                                                                                                                                                                                                                                                                          E: Fish & Richardson P.C.
225 Franklin Street
                                                                                                                                                                                                                                                                  Sequence 3, Application US/08920095
Patent No. 5837240
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 225 Fr
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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US-08-920-095-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGWVVFSEMGDSNASVPTPQPVYYREMFGHH 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IND PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

COMPUTER: IEM PC compatible

SOFTWARE: Batentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/466,248

FILING DATE: 06-7UN-1995

CLASSIFICATION NUMBER: US 08/447,177

FILING DATE: 19-MAY-1995

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/447,177

FILING DATE: 19-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 08/432,697

FILING DATE: 02-MAY-1995

CLASSIFICATION: 435

CLASSIFICATION: 435

RELING DATE: 02-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.5%; Score 2294; DB 2; Best Local Similarity 73.4%; Pred. No. 2.1e-213; Matches 416; Conservative 76; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERBYCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
SEE: Dunner
: 1300 I Street, N.W.
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           569 amino acids
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MOLECULE TYPE: protein
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  ADDRESSEE:
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US-08-466-248-26
                                                          STATE: D
COUNTRY:
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303 TIPFTVNTEAEHMDMLMVCHHLDXSIKEDVQFADSRIRPQTIAAEDTLHDMGIFSITSSD 362
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                                                                                                  62 ENTLDLVITNAMIIDYTGIYKADIGIKNGKIHGIGKAGNKDMQDGVSPHMVVGVGTEALA 121
                                                                                                                                                                     122 GEGMIITAGGIDSHTHFLSPQQPPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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                                                                                                                     182 LRAAEEYSMINGFLGKGNSSSKKOLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD
                                                                                                                                                                                                                                                       302 TIPYTINTVAEHLDMLMTCHHLDKRIREDLQFSQSRIRPGSIAAEDVLHDMGVIAMTSSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SQAMGRAGEVIPRIWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                               2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
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APPLICANT: Londono-Arcila, Patricia
APPLICANT: Londono-Arcila, Patricia
APPLICANT: Freeman, Donna
TITLE OF INVENTION: Use of salmonella vectors for
TITLE OF INVENTION: vaccination against helicobacter infection
FILE REFERENCE: 06132/060001
CURRENT APPLICATION NUMBER: US/09/431,705
CURRENT FILING DATE: 1999-11-01
NUMBER OF SEQ ID NOS: 52
SOFTWARE: FastSEQ for Windows Version 4.0
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 Mismatches
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543 YHVFVDGKEVTSKPANKVSLAQLF 566
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75;
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US-09-431-705-5
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Best Local Similarity 73.0%
Matches 414; Conservative
 Conservative
 415;
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LENGTH: 570
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 VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITMAGELNILPSSTTP 301
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                                                                                                                                       SQAMGRAGEVIPRTWQTADKNKKEFGKLPEDGKDNDNFRIKRYISKYTINPALTHGVSEY
                                                                                                                                                                                                        1GSVEEGK1ADLVVWNPAFFGVKPK1V1KGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application PC/TUS9605800
GENERAL INFORMATION:
APPLICANT: Oravax, Inc.
TITLE OF INVENTION: MULTIMERIC, RECOMBINANT UREASE VACCINE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/ACENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/020001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8006
INFORMATION FOR SEQ ID NO: 3:
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543 YHVFVDGKEVTSKPANKVSLAQLF 566
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23-APR-1996
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APPLICATION NUMBER: 08/431,041
FILING DATE: 28-APR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/568,122
FILING DATE: 06-DEC-1995
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73.6%;
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amino acid
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LENGTH: 566 amino acid
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Best Local Similarity
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CITY: Boston
STATE: MA
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PCT-US96-05800-3
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Query Match 74.8%; Score 2244; DB 1; Best Local Similarity 72.5%; Pred. No. 1.5e-208; Matches 411; Conservative 71; Mismatches 85;
                                                 NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELECOMMUNICATION INFORMATION:
TELEFHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acids
TYPE: amino acid
STRANDEDNESS: single
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                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                    ), OTHER INFORMATION:
US-08-467-822-21
                                                                                                                                                                                                                                                                                                           NAME/KEY: Protein
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   FILING DATE: 02
CLASSIFICATION:
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APPLICANT: Labigne, Agnes
APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
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ADDRESSEE: Dunner
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MEDIUM TYPE: Rloppy disk
COMPUTER: ISP PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,822
FILING DATE: 06-JUN-1995
CLASSIPFCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAX-1995
CLASSIPFICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAX-1995
CLASSIPFICATION ATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAX-1995
CLASSIPFICATION DATA:
APPLICATION NUMBER: US 08/432,697
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544 YHVFVDGKEVTSKPANKVSLAQLFSIF
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US-08-467-822-21
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                                                         Gaps
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Length 569;
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241 242

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APPLICANT: Labigne, Agnes
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sauerbaum, Sebastien
APPLICANT: Sterrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPONDENCES: 4
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                        363 SQAMGRVGEVITRTMQTADKOKKEFGRLKEEKGDNDNFRIKRYISKYTINPGIAHGISDY 422
                                                                                                                                                                                          GKAKFDISITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT 541
IGSVEEGKIADLVVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGHH
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APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION 435
PRIOR APPLICATION UMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION WIMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION WIMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REFERENCE/POCKET NUMBER: 25,146
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REFERENCE/POCKET NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                       543 YKVKVDGKEVTSKAADELSLAQLYNLF 569
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Patent No. 6258359
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 569 amino acids
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Florm:
COMPUTED
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LOCATION: 1..569
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                          APPLICANT: Ferrero, Richard L.
APPLICANT: Thiberge, Jean-Michel
TITLE OF INVENTION: IMMUNGENIC COMPOSITIONS AGAINST
TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE
TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID
TITLE OF INVENTION: POLYPEPTIDES
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD 241
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                                                                                                                                                                                                                                                                                                               STATE: D.C.
COUNTRY: USA
ZIP: COLON-1315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REPERBENCE/DOCKET NUMBER: 03495.0137-00000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 408-4400
INFORMATION FOR SEQ ID NO: 21:
SEQUIENCE CHARACTERISTICS:
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OTHER INFORMATION: /note= "URE B - FIGURE 3."
US-08-432-697-21
         Sauerbaum, Sebastien
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Matches 411; Conservative
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STRANDEDNESS: si
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                   61
                                  122 GEGMIITAGGIDSHTHFLSPQQFFTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM
                                                                                                                                                                                     123 AEGLIVTAGGIDTHIHFISPQQIPTAFASGVTTMIGGGTGPADGTWATTITPGRANLKSM
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                 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
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; Sequence 8, Application US/09338920B
; Patent No. 6709851
; GENERAL INPORMATION:
; APPLICANT: Soman, Gopalan
; APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
; TILE OF INVENTION: Stabilization of Helicobacter Urease
; TILE REFERENCE: 06132/02302
; CURRENT FILING DATE: 2002-12-23
; PRIOR PILIAGION NUMBER: US/09/338,920B
; PRIOR PILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 4.0
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; ORGANISM: Helicobacter pylori
US-09-338-920B-8
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US-09-338-920B-8
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                                                                                                                           2 KMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSPD
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                                                                                       85; Indels
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APPLICANT: Thomas, William D., Jr.
APPLICANT: Thomas, William D., Jr.
APPLICANT: Monath, Thomas P.
TITLE OF INVENTION: Stabilization of Helicobacter Urease
FILE REFERENCE: 06132/023002
CURRENT APPLICATION NUMBER: US/09/338,920B
CURRENT FILING DATE: 2002-12-23
FRIOR FILING DATE: 1997-09-12
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                                                   Query Match 74.8%; Score 2244; DB 2; Best Local Similarity 72.5%; Pred. No. 1.5e-208; Matches 411; Conservative 71; Mismatches 85;
/note= "URE B - FIGURE 3.
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SOSTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
IENGTH: 569
TYPE: PRT
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Patent No. 6709851
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US-09-338-920B-10
OTHER INFORMATION:
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US-08-466-248-21
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                                                             LRAAEEYSMNVGFLGKGNSSSKKQLVEQVEAGAIGFKLHEDWGTTPSAIDHCLSVADEYD 241
                                                                                                                                                              VQVCIHTDTVNEAGYVDDTLNAMNGRAIHAYHIEGAGGGHSPDVITWAGELNILPSSTTP 301
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                                                                                                                   GKAKFDTSITFVSKVAYENGVKEKLGLERQVLPVKNCRNITKKDFKFNDKTAKITVDPKT
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STREET: 600 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/07732242C
Patent No. 5298399
GENERAL INFORMATION
APPLICANT: Uczumi, Takeshi; Masaki, Haruhiko;
APPLICANT: Hidaka, Makoto; Nakamura, Akira;
APPLICANT: Maeda, Michihisa; Yoneta, Yasuo
TITLE OF INVENTION: Gene of Urease
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: New York
COUNTRY: USA
ZIP: 10016-2088
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 0.72mb
COMPUTER: IBM PC compatible (NEC PC-9801 RX)
OPERATING SYSTEM: MS DOS
SOFTWARE: ASCII Form
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/732,242C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 17081
REFERENCE/DOCKET NUMBER: 910532/HG
TELECOMUNICATION INFORMATION:
TELEPHONE: (212)972-1400
TELEPAX: (212)370-1622
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPN 2-210178
FILING DATE: 10-AUG-1990
ATTORNEY/AGENT INFORMATION:
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TELEX: 236268
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Sequence 26887, Application US/09252991A

Sequence 26887, Application US/09252991A

Sequence 26887, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: MUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO SEQUENCES

CURRENT PERERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEDENT: 566

TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                         122 GEGMIITAGGIDSHTHFLSPQQFPTALANGVTTMFGGGTGPVDGTNATTITPGKWNLHRM 181
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                                                                                                                                                                                                                    DB 1; Length 568;
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                                                                                                                                                                                                                  67.6%; Score 2028.5; DB 1; 66.1%; Pred. No. 1.2e-187; ative 77; Mismatches 112;
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                                             LENCTH: 568 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
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Matches 375; Conservative
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                    MOLECULE TYPE: peptide
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US-09-252-991A-26887
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421 YIGSVEEGKIADLUVWNPAFFGVKPKIVIKGGMVVFSEMGDSNASVPTPQPVYYREMFGH 480
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                                                                      1 MKMKKQEYVNTYGPTKGDKVRLGDTDLWAEVEHDYTTYGEELKFGAGKTIREGMGQSNSP 60
                                           Gaps
                                           7
                          Length 566;
                         Query Match
61.0%; Score 1828; DB 2; Length 56
Best Local Similarity 59.2%; Pred. No. 3.5e-168;
Matches 336; Conservative 67; Mismatches 143; Indels
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US-09-252-991A-26887
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